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(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM																											
(57) Abstract The present invention provides secreted proteins and polynucleotides encoding them, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.																											

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SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

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This application is a continuation-in-part of the following applications:

- (1) application Ser. No. 09/298,733, filed April 23, 1999; which claims the benefit of provisional application Ser. No. 60/082,961, filed April 24, 1998, now abandoned;
 - (2) provisional application Ser. No. 60/120,680, filed February 19, 1999;
 - 15 (3) provisional application Ser. No. 60/149,639, filed August 17, 1999;
 - (4) provisional application Ser. No. 60/155,686, filed September 23, 1999;
 - (5) provisional application Ser. No. 60/157,247, filed October 1, 1999;
 - (6) provisional application Ser. No. 60/167,823, filed November 29, 1999;
 - (7) provisional application Ser. No. 60/167,822, filed November 29, 1999;
 - 20 (8) provisional application Ser. No. 60/XXX,XXX, filed February 15, 2000;
- all of which are incorporated by reference herein.

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FIELD OF THE INVENTION

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

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BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 737 to nucleotide 5302;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 782 to nucleotide 5302;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb24_1 deposited with the ATCC under accession number 207113;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb24_1 deposited with the ATCC under accession number
15 207113;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb24_1 deposited with the ATCC under accession number 207113;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone vb24_1 deposited with the ATCC under accession number 207113;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:2;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 737 to nucleotide 5302; the nucleotide sequence of SEQ ID NO:1 from nucleotide 782 to nucleotide 5302; the nucleotide sequence of the full-length protein coding sequence of clone vb24_1 deposited with the ATCC under accession number 207113; or the nucleotide sequence of a mature protein coding sequence of clone vb24_1 deposited with the ATCC under accession number 207113. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb24_1 deposited with the ATCC under accession number 207113. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 756 to amino acid 765 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vb24_1 deposited with the ATCC under accession number 207113;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vb24_1 deposited with the ATCC under accession number 207113;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 737 to nucleotide 5302, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 737 to nucleotide 5302, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 737 to nucleotide 5302. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 782 to nucleotide 5302, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 782 to nucleotide 5302, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 782 to nucleotide 5302.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:2;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vb24_1 deposited with the ATCC under accession number 207113;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 15 ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 756 to amino acid 765 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:3;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 60 to nucleotide 1130;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 156 to nucleotide 1130;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc64_1 deposited with the ATCC under accession number 207113;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc64_1 deposited with the ATCC under accession number
30 207113;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc64_1 deposited with the ATCC under accession number 207113;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc64_1 deposited with the ATCC under accession number 207113;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 60 to nucleotide 1130; the nucleotide sequence of SEQ ID NO:3 from nucleotide 156 to nucleotide 1130; the nucleotide sequence of the full-length protein coding sequence of clone vc64_1 deposited with the ATCC under accession number 207113; or the nucleotide sequence of a mature protein coding sequence of clone vc64_1

deposited with the ATCC under accession number 207113. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc64_1 deposited with the ATCC under accession number 207113. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 173 to amino acid 182 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

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(aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(ab) the nucleotide sequence of the cDNA insert of clone vc64_1 deposited with the ATCC under accession number 207113;

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(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

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(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone vc64_1 deposited with the ATCC under accession number 207113;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

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(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 60 to nucleotide 1130, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 60 to nucleotide 1130, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 60 to nucleotide 1130. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 156 to nucleotide 1130, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 156 to nucleotide 1130, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 156 to nucleotide 1130.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
- (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc64_1 deposited with the ATCC under accession number 207113;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 173 to amino acid 182 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 195 to nucleotide 1298;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 333 to nucleotide 1298;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp20_1 deposited with the ATCC under accession number 207113;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp20_1 deposited with the ATCC under accession number 207113;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp20_1 deposited with the ATCC under accession number 207113;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp20_1 deposited with the ATCC under accession number 207113;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5
5 from nucleotide 195 to nucleotide 1298; the nucleotide sequence of SEQ ID NO:5 from nucleotide 333 to nucleotide 1298; the nucleotide sequence of the full-length protein coding sequence of clone vp20_1 deposited with the ATCC under accession number 207113; or the nucleotide sequence of a mature protein coding sequence of clone vp20_1 deposited with the ATCC under accession number 207113. In other preferred
10 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp20_1 deposited with the ATCC under accession number 207113. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more
15 preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 179 to amino acid 188 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
20 ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
30 vp20_1 deposited with the ATCC under accession number 207113;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vp20_1 deposited with the ATCC under accession number 207113;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 195 to nucleotide 1298, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 195 to nucleotide 1298, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 195 to nucleotide 1298. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 333 to nucleotide 1298, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 333 to nucleotide 1298, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 333 to nucleotide 1298.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
- 5 (b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vp20_1 deposited with the ATCC under accession number 207113;

the protein being substantially free from other mammalian proteins. Preferably such
10 protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ
15 ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 179 to amino acid 188 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 129 to nucleotide 731;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 186 to nucleotide 731;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq4_1 deposited with the ATCC under accession number 207113;
- (e) a polynucleotide encoding the full-length protein encoded by the
cDNA insert of clone vq4_1 deposited with the ATCC under accession number
30 207113;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq4_1 deposited with the ATCC under accession number 207113;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq4_1 deposited with the ATCC under accession number 207113;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 129 to nucleotide 731; the nucleotide sequence of SEQ ID NO:7 from nucleotide 186 to nucleotide 731; the nucleotide sequence of the full-length protein coding sequence of clone vq4_1 deposited with the ATCC under accession number 207113; or the nucleotide sequence of a mature protein coding sequence of clone vq4_1 deposited with
25 the ATCC under accession number 207113. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq4_1 deposited with the ATCC under accession number 207113. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological
30 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological

activity, the fragment comprising the amino acid sequence from amino acid 95 to amino acid 104 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(ab) the nucleotide sequence of the cDNA insert of clone vq4_1 deposited with the ATCC under accession number 207113;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:7, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:7; and

(bb) the nucleotide sequence of the cDNA insert of clone vq4_1 deposited with the ATCC under accession number 207113;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 129 to nucleotide 731, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 129 to nucleotide 731, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 129 to nucleotide 731. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 186 to nucleotide 731, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 186 to nucleotide 731, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 186 to nucleotide 731.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq4_1 deposited with the ATCC under accession number 207113;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 95 to amino acid 104 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 143 to nucleotide 571;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 221 to nucleotide 571;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo7_1 deposited with the ATCC under
10 accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo7_1 deposited with the ATCC under accession number PTA-362;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo7_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo7_1 deposited with the ATCC under accession number PTA-362;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any
30 one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:9.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9
5 from nucleotide 143 to nucleotide 571; the nucleotide sequence of SEQ ID NO:9 from nucleotide 221 to nucleotide 571; the nucleotide sequence of the full-length protein coding sequence of clone vo7_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo7_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the
10 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo7_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably
15 thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 66 to amino acid 75 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
20 ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
30 vo7_1 deposited with the ATCC under accession number PTA-362;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vo7_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 143 to nucleotide 571, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 143 to nucleotide 571, to a nucleotide sequence

20 corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 143 to nucleotide 571. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 221 to nucleotide 571, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide

25 221 to nucleotide 571, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 221 to nucleotide 571.

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In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo7_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 66 to amino acid 75 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 112 to nucleotide 570;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 190 to nucleotide 570;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc65_1 deposited with the ATCC under accession number PTA-361;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc65_1 deposited with the ATCC under accession number
- 30 PTA-361;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc65_1 deposited with the ATCC under accession number PTA-361;
- 5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc65_1 deposited with the ATCC under accession number PTA-361;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- 10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:11.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 112 to nucleotide 570; the nucleotide sequence of SEQ ID NO:11 from nucleotide 190 to nucleotide 570; the nucleotide sequence of the full-length protein coding sequence of clone vc65_1 deposited with the ATCC under accession number PTA-361; or the nucleotide sequence of a mature protein coding sequence of clone vc65_1
- 25 deposited with the ATCC under accession number PTA-361. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc65_1 deposited with the ATCC under accession number PTA-361. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12
- 30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 71 to amino acid 80 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(ab) the nucleotide sequence of the cDNA insert of clone vc65_1 deposited with the ATCC under accession number PTA-
15 361;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(bb) the nucleotide sequence of the cDNA insert of clone vc65_1 deposited with the ATCC under accession number PTA-
361;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 112 to nucleotide 570, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 112 to nucleotide 570, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 112 to nucleotide 570. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 190 to nucleotide 570, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 190 to nucleotide 570, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 190 to nucleotide 570.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vc65_1 deposited with the ATCC under accession number PTA-361;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 71 to amino acid 80 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 4 to nucleotide 261;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:13 from nucleotide 124 to nucleotide 261;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc66_1 deposited with the ATCC under accession number PTA-361;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vc66_1 deposited with the ATCC under accession number PTA-361;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc66_1 deposited with the ATCC under accession number PTA-361;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc66_1 deposited with the ATCC under accession number PTA-361;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 4 to nucleotide 261; the nucleotide sequence of SEQ ID NO:13 from nucleotide 124 to nucleotide 261; the nucleotide sequence of the full-length protein coding sequence of clone vc66_1 deposited with the ATCC under accession number PTA-361; or the nucleotide sequence of a mature protein coding sequence of clone vc66_1 deposited with the ATCC under accession number PTA-361. In other preferred
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embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc66_1 deposited with the ATCC under accession number PTA-361. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a
polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.
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Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
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in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(ab) the nucleotide sequence of the cDNA insert of clone
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vc66_1 deposited with the ATCC under accession number PTA-361;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(bb) the nucleotide sequence of the cDNA insert of clone vc66_1 deposited with the ATCC under accession number PTA-361;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
25 corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 4 to nucleotide 261, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 4 to nucleotide 261, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 4 to nucleotide 261. Also preferably the polynucleotide isolated according to the above
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 124 to nucleotide 261, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from

nucleotide 124 to nucleotide 261, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 124 to nucleotide 261.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 vc66_1 deposited with the ATCC under accession number PTA-361;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 135 to nucleotide 1227;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:15 from nucleotide 216 to nucleotide 1227;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc68_1 deposited with the ATCC under accession number PTA-361;
- (e) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone vc68_1 deposited with the ATCC under accession number PTA-361;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc68_1 deposited with the ATCC under accession number PTA-361;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc68_1 deposited with the ATCC under accession number PTA-361;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:15.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 135 to nucleotide 1227; the nucleotide sequence of SEQ ID NO:15 from nucleotide 216 to nucleotide 1227; the nucleotide sequence of the full-length protein coding sequence of clone vc68_1 deposited with the ATCC under accession number PTA-361; or the nucleotide sequence of a mature protein coding sequence of clone vc68_1 deposited with the ATCC under accession number PTA-361. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc68_1 deposited with the ATCC under accession number PTA-361. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 160 to amino acid 169 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(ab) the nucleotide sequence of the cDNA insert of clone vc68_1 deposited with the ATCC under accession number PTA-
15 361;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(bb) the nucleotide sequence of the cDNA insert of clone vc68_1 deposited with the ATCC under accession number PTA-
30 361;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 135 to nucleotide 1227, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 135 to nucleotide 1227, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 135 to nucleotide 1227. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 216 to nucleotide 1227, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 216 to nucleotide 1227, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 216 to nucleotide 1227.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
- (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc68_1 deposited with the ATCC under accession number PTA-361;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 160 to amino acid 169 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 79 to nucleotide 2424;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:17 from nucleotide 145 to nucleotide 2424;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vk6_1 deposited with the ATCC under accession number PTA-361;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vk6_1 deposited with the ATCC under accession number PTA-361;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vk6_1 deposited with the ATCC under accession number PTA-361;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vk6_1 deposited with the ATCC under accession number PTA-361;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 79 to nucleotide 2424; the nucleotide sequence of SEQ ID NO:17 from nucleotide 145 to nucleotide 2424; the nucleotide sequence of the full-length protein coding sequence of clone vk6_1 deposited with the ATCC under accession number PTA-361; or the nucleotide sequence of a mature protein coding sequence of clone vk6_1 deposited with the ATCC under accession number PTA-361. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vk6_1 deposited with the ATCC under accession number PTA-361. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 386 to amino acid 395 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vk6_1 deposited with the ATCC under accession number PTA-361;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vk6_1 deposited with the ATCC under accession number PTA-361;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 79 to nucleotide 2424, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 79 to nucleotide 2424, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 79 to nucleotide 2424. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 145 to nucleotide 2424, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from
30 nucleotide 145 to nucleotide 2424, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 145 to nucleotide 2424.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vk6_1 deposited with the ATCC under accession number PTA-361;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 386 to amino acid 395 of SEQ ID NO:18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:19;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 2 to nucleotide 733;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 71 to nucleotide 733;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo4_1 deposited with the ATCC under accession number PTA-361;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 30 cDNA insert of clone vo4_1 deposited with the ATCC under accession number PTA-361;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo4_1 deposited with the ATCC under accession number PTA-361;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo4_1 deposited with the ATCC under accession number PTA-361;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:19.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 2 to nucleotide 733; the nucleotide sequence of SEQ ID NO:19 from nucleotide 71 to nucleotide 733; the nucleotide sequence of the full-length protein coding sequence of clone vo4_1 deposited with the ATCC under accession number PTA-361; or the nucleotide sequence of a mature protein coding sequence of clone vo4_1

25 deposited with the ATCC under accession number PTA-361. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo4_1 deposited with the ATCC under accession number PTA-361. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20
30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(ab) the nucleotide sequence of the cDNA insert of clone vo4_1 deposited with the ATCC under accession number PTA-361;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(bb) the nucleotide sequence of the cDNA insert of clone vo4_1 deposited with the ATCC under accession number PTA-361;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 2 to nucleotide 733, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 2 to nucleotide 733, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 2 to nucleotide 733. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 71 to nucleotide 733, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide
15 71 to nucleotide 733, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 71 to nucleotide 733.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:20;
(b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
(c) the amino acid sequence encoded by the cDNA insert of clone vo4_1 deposited with the ATCC under accession number PTA-361;

25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:20; or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 151 to nucleotide 1323;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 217 to nucleotide 1323;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo8_1 deposited with the ATCC under accession number PTA-361;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo8_1 deposited with the ATCC under accession number PTA-361;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo8_1 deposited with the ATCC under accession number PTA-361;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo8_1 deposited with the ATCC under accession number PTA-361;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 151 to nucleotide 1323; the nucleotide sequence of SEQ ID NO:21 from nucleotide 217 to nucleotide 1323; the nucleotide sequence of the full-length protein coding sequence of clone vo8_1 deposited with the ATCC under accession number PTA-361; or the nucleotide sequence of a mature protein coding sequence of clone vo8_1 deposited with the ATCC under accession number PTA-361. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo8_1 deposited with the ATCC under accession number PTA-361. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 190 to amino acid 199 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vo8_1 deposited with the ATCC under accession number PTA-361;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vo8_1 deposited with the ATCC under accession number PTA-361;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 151 to nucleotide 1323, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 151 to nucleotide 1323, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 151 to nucleotide 1323. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 217 to nucleotide 1323, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from
30 nucleotide 217 to nucleotide 1323, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 217 to nucleotide 1323.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
- 5 (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo8_1 deposited with the ATCC under accession number PTA-361;

the protein being substantially free from other mammalian proteins. Preferably such
10 protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ
15 ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 190 to amino acid 199 of SEQ ID NO:22.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 20 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 134 to nucleotide 613;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 215 to nucleotide 613;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo10_1 deposited with the ATCC under accession number PTA-361;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo10_1 deposited with the ATCC under accession number
30 PTA-361;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo10_1 deposited with the ATCC under accession number PTA-361;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo10_1 deposited with the ATCC under accession number PTA-361;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:23.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 134 to nucleotide 613; the nucleotide sequence of SEQ ID NO:23 from nucleotide 215 to nucleotide 613; the nucleotide sequence of the full-length protein coding sequence of clone vo10_1 deposited with the ATCC under accession number PTA-361; or the nucleotide sequence of a mature protein coding sequence of clone vo10_1
25 deposited with the ATCC under accession number PTA-361. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo10_1 deposited with the ATCC under accession number PTA-361. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24
30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 75 to amino acid 84 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(ab) the nucleotide sequence of the cDNA insert of clone vo10_1 deposited with the ATCC under accession number PTA-
15 361;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);
20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone vo10_1 deposited with the ATCC under accession number PTA-
25 361;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and
30

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 134 to nucleotide 613, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 134 to nucleotide 613, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 134 to nucleotide 613. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 215 to nucleotide 613, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 215 to nucleotide 613, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 215 to nucleotide 613.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:24;
- (b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo10_1 deposited with the ATCC under accession number PTA-361;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 75 to amino acid 84 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 102 to nucleotide 1163;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:25 from nucleotide 156 to nucleotide 1163;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo20_1 deposited with the ATCC under accession number PTA-361;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vo20_1 deposited with the ATCC under accession number PTA-361;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo20_1 deposited with the ATCC under accession number PTA-361;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone vo20_1 deposited with the ATCC under accession number PTA-361;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 102 to nucleotide 1163; the nucleotide sequence of SEQ ID NO:25 from nucleotide 156 to nucleotide 1163; the nucleotide sequence of the full-length protein coding sequence of clone vo20_1 deposited with the ATCC under accession number PTA-361; or the nucleotide sequence of a mature protein coding sequence of clone vo20_1 deposited with the ATCC under accession number PTA-361. In other preferred
10 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo20_1 deposited with the ATCC under accession number PTA-361. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably
15 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 172 to amino acid 181 of SEQ ID NO:26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.
20 ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
30 vo20_1 deposited with the ATCC under accession number PTA-361;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(bb) the nucleotide sequence of the cDNA insert of clone vo20_1 deposited with the ATCC under accession number PTA-361;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

25 corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 102 to nucleotide 1163, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 102 to nucleotide 1163, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 102 to nucleotide 1163. Also preferably the polynucleotide isolated according to the above
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 156 to nucleotide 1163, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from

nucleotide 156 to nucleotide 1163, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 156 to nucleotide 1163.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:26;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 vo20_1 deposited with the ATCC under accession number PTA-361;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 172 to amino acid 181 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 67 to nucleotide 702;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:27 from nucleotide 157 to nucleotide 702;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo21_1 deposited with the ATCC under accession number PTA-361;
- (e) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone vo21_1 deposited with the ATCC under accession number PTA-361;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo21_1 deposited with the ATCC under accession number PTA-361;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo21_1 deposited with the ATCC under accession number PTA-361;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:27.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 67 to nucleotide 702; the nucleotide sequence of SEQ ID NO:27 from nucleotide 157 to nucleotide 702; the nucleotide sequence of the full-length protein coding sequence of clone vo21_1 deposited with the ATCC under accession number PTA-361; or the nucleotide sequence of a mature protein coding sequence of clone vo21_1

25 deposited with the ATCC under accession number PTA-361. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo21_1 deposited with the ATCC under accession number PTA-361. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28
30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 101 to amino acid 110 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(ab) the nucleotide sequence of the cDNA insert of clone vo21_1 deposited with the ATCC under accession number PTA-361;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(bb) the nucleotide sequence of the cDNA insert of clone vo21_1 deposited with the ATCC under accession number PTA-361;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 67 to nucleotide 702, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 67 to nucleotide 702, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 67 to nucleotide 702. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 157 to nucleotide 702, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 157 to nucleotide 702, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 157 to nucleotide 702.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo21_1 deposited with the ATCC under accession number PTA-361;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty; most preferably thirty) contiguous amino acids of SEQ ID NO:28; or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 101 to amino acid 110 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 57 to nucleotide 272;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:29 from nucleotide 114 to nucleotide 272;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp24_1 deposited with the ATCC under accession number PTA-361;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vp24_1 deposited with the ATCC under accession number PTA-361;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp24_1 deposited with the ATCC under accession number PTA-361;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp24_1 deposited with the ATCC under accession number PTA-361;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 57 to nucleotide 272; the nucleotide sequence of SEQ ID NO:29 from nucleotide 114 to nucleotide 272; the nucleotide sequence of the full-length protein coding sequence of clone vp24_1 deposited with the ATCC under accession number PTA-361; or the nucleotide sequence of a mature protein coding sequence of clone vp24_1 deposited with the ATCC under accession number PTA-361. In other preferred
5 NO:29 from nucleotide 57 to nucleotide 272; the nucleotide sequence of SEQ ID NO:29 from nucleotide 114 to nucleotide 272; the nucleotide sequence of the full-length protein coding sequence of clone vp24_1 deposited with the ATCC under accession number PTA-361; or the nucleotide sequence of a mature protein coding sequence of clone vp24_1 deposited with the ATCC under accession number PTA-361. In other preferred
10 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp24_1 deposited with the ATCC under accession number PTA-361. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably
15 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 31 to amino acid 40 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.
20 ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(ab) the nucleotide sequence of the cDNA insert of clone vp24_1 deposited with the ATCC under accession number PTA-361;
30 361;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(bb) the nucleotide sequence of the cDNA insert of clone vp24_1 deposited with the ATCC under accession number PTA-361;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
25 corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 57 to nucleotide 272, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 57 to nucleotide 272, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 57 to nucleotide 272. Also preferably the polynucleotide isolated according to the above
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 114 to nucleotide 272, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from

nucleotide 114 to nucleotide 272, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 114 to nucleotide 272.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 vp24_1 deposited with the ATCC under accession number PTA-361;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 31 to amino acid 40 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 38 to nucleotide 757;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:31 from nucleotide 137 to nucleotide 757;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo17_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone vo17_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo17_1 deposited with the ATCC under accession number PTA-366;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo17_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:31.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 38 to nucleotide 757; the nucleotide sequence of SEQ ID NO:31 from nucleotide 137 to nucleotide 757; the nucleotide sequence of the full-length protein coding sequence of clone vo17_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo17_1
25 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo17_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32
30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ab) the nucleotide sequence of the cDNA insert of clone vo17_1 deposited with the ATCC under accession number PTA-
15 366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(bb) the nucleotide sequence of the cDNA insert of clone vo17_1 deposited with the ATCC under accession number PTA-
30 366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 38 to nucleotide 757, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 38 to nucleotide 757, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 38 to nucleotide 757. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 137 to nucleotide 757, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 137 to nucleotide 757, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 137 to nucleotide 757.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;
- (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo17_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 93 to nucleotide 263;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:33 from nucleotide 174 to nucleotide 263;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq11_1 deposited with the ATCC under accession number PTA-367;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vq11_1 deposited with the ATCC under accession number PTA-367;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq11_1 deposited with the ATCC under accession number PTA-367;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq11_1 deposited with the ATCC under accession number PTA-367;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:33.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 93 to nucleotide 263; the nucleotide sequence of SEQ ID NO:33 from nucleotide 174 to nucleotide 263; the nucleotide sequence of the full-length protein coding sequence of clone vq11_1 deposited with the ATCC under accession number PTA-367; or the nucleotide sequence of a mature protein coding sequence of clone vq11_1 deposited with the ATCC under accession number PTA-367. In other preferred
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embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq11_1 deposited with the ATCC under accession number PTA-367. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.
20

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
30 vq11_1 deposited with the ATCC under accession number PTA-367;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(bb) the nucleotide sequence of the cDNA insert of clone vq11_1 deposited with the ATCC under accession number PTA-367;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

25 corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 93 to nucleotide 263, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 93 to nucleotide 263, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 93 to nucleotide 263. Also preferably the polynucleotide isolated according to the above
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 174 to nucleotide 263, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from

nucleotide 174 to nucleotide 263, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 174 to nucleotide 263.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 vq11_1 deposited with the ATCC under accession number PTA-367;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 43 to nucleotide 1125;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:35 from nucleotide 85 to nucleotide 1125;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq12_1 deposited with the ATCC under accession number PTA-367;
- (e) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone vq12_1 deposited with the ATCC under accession number PTA-367;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq12_1 deposited with the ATCC under accession number PTA-367;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq12_1 deposited with the ATCC under accession number PTA-367;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:35.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 43 to nucleotide 1125; the nucleotide sequence of SEQ ID NO:35 from nucleotide 85 to nucleotide 1125; the nucleotide sequence of the full-length protein coding sequence of clone vq12_1 deposited with the ATCC under accession number PTA-367; or the nucleotide sequence of a mature protein coding sequence of clone vq12_1
25 deposited with the ATCC under accession number PTA-367. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq12_1 deposited with the ATCC under accession number PTA-367. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36
30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 175 to amino acid 184 of SEQ ID NO:36.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(ab) the nucleotide sequence of the cDNA insert of clone vq12_1 deposited with the ATCC under accession number PTA-
15 367;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(bb) the nucleotide sequence of the cDNA insert of clone vq12_1 deposited with the ATCC under accession number PTA-
25 367;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 43 to nucleotide 1125, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 43 to nucleotide 1125, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 43 to nucleotide 1125. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 85 to nucleotide 1125, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 85 to nucleotide 1125, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 85 to nucleotide 1125.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq12_1 deposited with the ATCC under accession number PTA-367;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 175 to amino acid 184 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 32 to nucleotide 904;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:37 from nucleotide 77 to nucleotide 904;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq14_1 deposited with the ATCC under accession number PTA-367;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vq14_1 deposited with the ATCC under accession number PTA-367;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq14_1 deposited with the ATCC under accession number PTA-367;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq14_1 deposited with the ATCC under accession number PTA-367;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:37.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 32 to nucleotide 904; the nucleotide sequence of SEQ ID NO:37 from nucleotide 77 to nucleotide 904; the nucleotide sequence of the full-length protein coding sequence of clone vq14_1 deposited with the ATCC under accession number PTA-367; or the nucleotide sequence of a mature protein coding sequence of clone vq14_1 deposited with the ATCC under accession number PTA-367. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq14_1 deposited with the ATCC under accession number PTA-367. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 140 to amino acid 149 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone vq14_1 deposited with the ATCC under accession number PTA-367;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(bb) the nucleotide sequence of the cDNA insert of clone vq14_1 deposited with the ATCC under accession number PTA-367;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
25 corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 32 to nucleotide 904, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 32 to nucleotide 904, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 32 to nucleotide 904. Also preferably the polynucleotide isolated according to the above
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 77 to nucleotide 904, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide

77 to nucleotide 904, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 77 to nucleotide 904.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 vq14_1 deposited with the ATCC under accession number PTA-367;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 140 to amino acid 149 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 384 to nucleotide 1193;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 642 to nucleotide 1193;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq15_1 deposited with the ATCC under accession number PTA-367;
- (e) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone vq15_1 deposited with the ATCC under accession number PTA-367;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq15_1 deposited with the ATCC under accession number PTA-367;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq15_1 deposited with the ATCC under accession number PTA-367;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:39.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 384 to nucleotide 1193; the nucleotide sequence of SEQ ID NO:39 from nucleotide 642 to nucleotide 1193; the nucleotide sequence of the full-length protein coding sequence of clone vq15_1 deposited with the ATCC under accession number PTA-367; or the nucleotide sequence of a mature protein coding sequence of clone vq15_1
25 deposited with the ATCC under accession number PTA-367. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq15_1 deposited with the ATCC under accession number PTA-367. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40
30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 130 to amino acid 139 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(ab) the nucleotide sequence of the cDNA insert of clone vq15_1 deposited with the ATCC under accession number PTA-
15 367;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(bb) the nucleotide sequence of the cDNA insert of clone vq15_1 deposited with the ATCC under accession number PTA-
30 367;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 384 to nucleotide 1193, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 384 to nucleotide 1193, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 384 to nucleotide 1193. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 642 to nucleotide 1193, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 642 to nucleotide 1193, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 642 to nucleotide 1193.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq15_1 deposited with the ATCC under accession number PTA-367;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 130 to amino acid 139 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 132 to nucleotide 503;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:41 from nucleotide 189 to nucleotide 503;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq17_1 deposited with the ATCC under accession number PTA-367;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vq17_1 deposited with the ATCC under accession number PTA-367;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq17_1 deposited with the ATCC under accession number PTA-367;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq17_1 deposited with the ATCC under accession number PTA-367;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 132 to nucleotide 503; the nucleotide sequence of SEQ ID NO:41 from nucleotide 189 to nucleotide 503; the nucleotide sequence of the full-length protein coding sequence of clone vq17_1 deposited with the ATCC under accession number PTA-367; or the nucleotide sequence of a mature protein coding sequence of clone vq17_1 deposited with the ATCC under accession number PTA-367. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq17_1 deposited with the ATCC under accession number PTA-367. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 57 to amino acid 66 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(ab) the nucleotide sequence of the cDNA insert of clone vq17_1 deposited with the ATCC under accession number PTA-367;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(bb) the nucleotide sequence of the cDNA insert of clone vq17_1 deposited with the ATCC under accession number PTA-367;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
25 corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 132 to nucleotide 503, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 132 to nucleotide 503, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 132 to nucleotide 503. Also preferably the polynucleotide isolated according to the above
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 189 to nucleotide 503, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from

nucleotide 189 to nucleotide 503, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 189 to nucleotide 503.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 vq17_1 deposited with the ATCC under accession number PTA-367;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 57 to amino acid 66 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 69 to nucleotide 401;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:43 from nucleotide 138 to nucleotide 401;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq18_1 deposited with the ATCC under accession number PTA-367;
- (e) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone vq18_1 deposited with the ATCC under accession number PTA-367;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq18_1 deposited with the ATCC under accession number PTA-367;
- 5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq18_1 deposited with the ATCC under accession number PTA-367;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;
- 10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:43.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 69 to nucleotide 401; the nucleotide sequence of SEQ ID NO:43 from nucleotide 138 to nucleotide 401; the nucleotide sequence of the full-length protein coding sequence of clone vq18_1 deposited with the ATCC under accession number PTA-367; or the nucleotide sequence of a mature protein coding sequence of clone vq18_1
- 25 deposited with the ATCC under accession number PTA-367. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq18_1 deposited with the ATCC under accession number PTA-367. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44
- 30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 50 to amino acid 59 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(ab) the nucleotide sequence of the cDNA insert of clone vq18_1 deposited with the ATCC under accession number PTA-
15 367;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(bb) the nucleotide sequence of the cDNA insert of clone vq18_1 deposited with the ATCC under accession number PTA-
25 367;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 69 to nucleotide 401, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 69 to nucleotide 401, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 69 to nucleotide 401. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 138 to nucleotide 401, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 138 to nucleotide 401, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 138 to nucleotide 401.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:44;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq18_1 deposited with the ATCC under accession number PTA-367;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 50 to amino acid 59 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 65 to nucleotide 1180;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:45 from nucleotide 149 to nucleotide 1180;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq22_1 deposited with the ATCC under accession number PTA-367;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vq22_1 deposited with the ATCC under accession number PTA-367;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq22_1 deposited with the ATCC under accession number PTA-367;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq22_1 deposited with the ATCC under accession number PTA-367;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 65 to nucleotide 1180; the nucleotide sequence of SEQ ID NO:45 from nucleotide 149 to nucleotide 1180; the nucleotide sequence of the full-length protein coding sequence of clone vq22_1 deposited with the ATCC under accession number PTA-367; or the nucleotide sequence of a mature protein coding sequence of clone vq22_1 deposited with the ATCC under accession number PTA-367. In other preferred
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embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq22_1 deposited with the ATCC under accession number PTA-367. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a
polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 181 to amino acid 190 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.
20

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
30 vq22_1 deposited with the ATCC under accession number PTA-367;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(bb) the nucleotide sequence of the cDNA insert of clone vq22_1 deposited with the ATCC under accession number PTA-367;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
25 corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 65 to nucleotide 1180, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 65 to nucleotide 1180, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 65 to nucleotide 1180. Also preferably the polynucleotide isolated according to the above
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 149 to nucleotide 1180, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from

nucleotide 149 to nucleotide 1180, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 149 to nucleotide 1180.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
- (b) a fragment of the amino acid sequence of SEQ ID NO:46, the
fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
10 vq22_1 deposited with the ATCC under accession number PTA-367;
the protein being substantially free from other mammalian proteins. Preferably such
protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred
embodiments, the present invention provides a protein comprising a fragment of the amino
acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ
ID NO:46 having biological activity, the fragment comprising the amino acid sequence
from amino acid 181 to amino acid 190 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:47;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:47 from nucleotide 18 to nucleotide 1409;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:47 from nucleotide 60 to nucleotide 1409;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
length protein coding sequence of clone vr3_1 deposited with the ATCC under
accession number PTA-367;
- (e) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone vr3_1 deposited with the ATCC under accession number
PTA-367;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vr3_1 deposited with the ATCC under accession number PTA-367;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vr3_1 deposited with the ATCC under accession number PTA-367;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 18 to nucleotide 1409; the nucleotide sequence of SEQ ID NO:47 from nucleotide 60 to nucleotide 1409; the nucleotide sequence of the full-length protein coding sequence of clone vr3_1 deposited with the ATCC under accession number PTA-367; or the nucleotide sequence of a mature protein coding sequence of clone vr3_1 deposited with the ATCC under accession number PTA-367. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vr3_1 deposited with the ATCC under accession number PTA-367. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 227 to amino acid 236 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:47, but excluding the poly(A) tail at the
3' end of SEQ ID NO:47; and

(ab) the nucleotide sequence of the cDNA insert of clone
vr3_1 deposited with the ATCC under accession number PTA-367;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize
in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
consisting of:

25 (ba) SEQ ID NO:47, but excluding the poly(A) tail at the
3' end of SEQ ID NO:47; and

(bb) the nucleotide sequence of the cDNA insert of clone
vr3_1 deposited with the ATCC under accession number PTA-367;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 18 to nucleotide 1409, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 18 to nucleotide 1409, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 18 to nucleotide 1409. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 60 to nucleotide 1409, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from
15 nucleotide 60 to nucleotide 1409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 60 to nucleotide 1409.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:48;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vr3_1 deposited with the ATCC under accession number PTA-367;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 227 to amino acid 236 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 690 to nucleotide 2570;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 765 to nucleotide 2570;
- 10 (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 1286 to nucleotide 2895;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb26_1 deposited with the ATCC under accession number PTA-501;
- 15 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb26_1 deposited with the ATCC under accession number PTA-501;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb26_1 deposited with the ATCC under accession number PTA-501;
- 20 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb26_1 deposited with the ATCC under accession number PTA-501;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- 25 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- 30 (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 690 to nucleotide 2570; the nucleotide sequence of SEQ ID NO:49 from nucleotide 765 to nucleotide 2570; the nucleotide sequence of SEQ ID NO:49 from nucleotide 1286 to nucleotide 2895; the nucleotide sequence of SEQ ID NO:49 from nucleotide 1286 to nucleotide 2570; the nucleotide sequence of SEQ ID NO:49 from nucleotide 981 to nucleotide 1282; the nucleotide sequence of the full-length protein coding sequence of clone vb26_1 deposited with the ATCC under accession number PTA-501; or the nucleotide sequence of a mature protein coding sequence of clone vb26_1 deposited with the ATCC under accession number PTA-501. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb26_1 deposited with the ATCC under accession number PTA-501. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50 from amino acid 112 to amino acid 197. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising an amino acid sequence selected from the group comprising the sequence from amino acid 308 to amino acid 317 of SEQ ID NO:50, the sequence from amino acid 112 to amino acid 197 of SEQ ID NO:50, the sequence from amino acid 200 to amino acid 627 of SEQ ID NO:50, and the sequence from amino acid 364 to amino acid 373 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(ab) the nucleotide sequence of the cDNA insert of clone vb26_1 deposited with the ATCC under accession number PTA-501;

10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

15 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(bb) the nucleotide sequence of the cDNA insert of clone vb26_1 deposited with the ATCC under accession number PTA-501;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 690 to nucleotide 2570, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 690 to nucleotide 2570, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 690 to nucleotide 2570. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 765 to nucleotide 2570, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 765 to nucleotide 2570, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 765 to nucleotide 2570. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 1286 to nucleotide 2895, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 1286 to nucleotide 2895, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 1286 to nucleotide 2895.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
- (b) the amino acid sequence of SEQ ID NO:50 from amino acid 112 to amino acid 197;
- (c) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
- (d) the amino acid sequence encoded by the cDNA insert of clone vb26_1 deposited with the ATCC under accession number PTA-501;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50 or the amino acid sequence of SEQ ID NO:50 from amino acid 112 to amino acid 197. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising an amino acid sequence selected from the group comprising the sequence from amino acid 308 to amino acid 317 of SEQ ID NO:50, the sequence from amino acid 112 to amino acid 197 of SEQ ID NO:50, the sequence from amino acid 200 to amino acid 627 of SEQ ID NO:50, and the sequence from amino acid 364 to amino acid 373 of SEQ ID NO:50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 105 to nucleotide 1724;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1724;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc70_1 deposited with the ATCC under accession number PTA-1074;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc70_1 deposited with the ATCC under accession number
20 PTA-1074;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc70_1 deposited with the ATCC under accession number PTA-1074;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
25 insert of clone vc70_1 deposited with the ATCC under accession number PTA-1074;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (i) a polynucleotide encoding a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:51.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 105 to nucleotide 1724; the nucleotide sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1724; the nucleotide sequence of the full-length protein coding sequence of clone vc70_1 deposited with the ATCC under accession number PTA-1074; or the nucleotide sequence of a mature protein coding sequence of clone vc70_1
15 deposited with the ATCC under accession number PTA-1074. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc70_1 deposited with the ATCC under accession number PTA-1074. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52
20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 265 to amino acid 274 of SEQ ID NO:52.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(ab) the nucleotide sequence of the cDNA insert of clone vc70_1 deposited with the ATCC under accession number PTA-1074;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

10 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(bb) the nucleotide sequence of the cDNA insert of clone vc70_1 deposited with the ATCC under accession number PTA-1074;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a

nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 105 to nucleotide 1724, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 105 to nucleotide 1724, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 105 to nucleotide 1724. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1724, and extending contiguously from a
5 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1724, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1724.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
10 consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
- (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
15 vc70_1 deposited with the ATCC under accession number PTA-1074;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably
20 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 265 to amino acid 274 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an
25 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 3 to nucleotide 239;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo28_1 deposited with the ATCC under
30 accession number PTA-1074;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo28_1 deposited with the ATCC under accession number PTA-1074;

5 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo28_1 deposited with the ATCC under accession number PTA-1074;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo28_1 deposited with the ATCC under accession number PTA-1074;

10 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

15 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
25 NO:53 from nucleotide 3 to nucleotide 239; the nucleotide sequence of the full-length protein coding sequence of clone vo28_1 deposited with the ATCC under accession number PTA-1074; or the nucleotide sequence of a mature protein coding sequence of clone vo28_1 deposited with the ATCC under accession number PTA-1074. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein
30 encoded by the cDNA insert of clone vo28_1 deposited with the ATCC under accession number PTA-1074. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid
5 sequence from amino acid 34 to amino acid 43 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 15 (aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and
- (ab) the nucleotide sequence of the cDNA insert of clone vo28_1 deposited with the ATCC under accession number PTA-1074;
- (ii) hybridizing said probe(s) to human genomic DNA in
20 conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- 25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and
- 30 (bb) the nucleotide sequence of the cDNA insert of clone vo28_1 deposited with the ATCC under accession number PTA-1074;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv,) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 3 to nucleotide 239, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 3 to nucleotide 239, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide
15 3 to nucleotide 239.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:54;
- 20 (b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo28_1 deposited with the ATCC under accession number PTA-1074;

the protein being substantially free from other mammalian proteins. Preferably such
25 protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ
30 ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 49 to nucleotide 1452;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 109 to nucleotide 1452;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo29_1 deposited with the ATCC under accession number PTA-1074;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo29_1 deposited with the ATCC under accession number PTA-1074;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo29_1 deposited with the ATCC under accession number PTA-1074;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo29_1 deposited with the ATCC under accession number PTA-20 1074;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment 25 comprising eight contiguous amino acids of SEQ ID NO:56;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 49 to nucleotide 1452; the nucleotide sequence of SEQ ID NO:55 from nucleotide 109 to nucleotide 1452; the nucleotide sequence of the full-length protein coding sequence of clone vo29_1 deposited with the ATCC under accession number PTA-1074; or the nucleotide sequence of a mature protein coding sequence of clone vo29_1 deposited with the ATCC under accession number PTA-1074. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo29_1 deposited with the ATCC under accession number PTA-1074. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 229 to amino acid 238 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(ab) the nucleotide sequence of the cDNA insert of clone vo29_1 deposited with the ATCC under accession number PTA-1074;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(bb) the nucleotide sequence of the cDNA insert of clone vo29_1 deposited with the ATCC under accession number PTA-1074;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
25 corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 49 to nucleotide 1452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 49 to nucleotide 1452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 49 to nucleotide 1452. Also preferably the polynucleotide isolated according to the above
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 109 to nucleotide 1452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from

nucleotide 109 to nucleotide 1452; to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 109 to nucleotide 1452.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:56;
- (b) a fragment of the amino acid sequence of SEQ ID NO:56, the
fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
10 vo29_1 deposited with the ATCC under accession number PTA-1074;
the protein being substantially free from other mammalian proteins. Preferably such
protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred
embodiments, the present invention provides a protein comprising a fragment of the amino
acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ
ID NO:56 having biological activity, the fragment comprising the amino acid sequence
from amino acid 229 to amino acid 238 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:57;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:57 from nucleotide 48 to nucleotide 866;
- 25 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:57 from nucleotide 114 to nucleotide 866;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
length protein coding sequence of clone vo30_1 deposited with the ATCC under
accession number PTA-1074;
- 30 (e) a polynucleotide encoding the full-length protein encoded by the
cDNA insert of clone vo30_1 deposited with the ATCC under accession number
PTA-1074;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo30_1 deposited with the ATCC under accession number PTA-1074;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo30_1 deposited with the ATCC under accession number PTA-1074;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

15 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:57.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 48 to nucleotide 866; the nucleotide sequence of SEQ ID NO:57 from nucleotide 114 to nucleotide 866; the nucleotide sequence of the full-length protein coding sequence of clone vo30_1 deposited with the ATCC under accession number PTA-25 1074; or the nucleotide sequence of a mature protein coding sequence of clone vo30_1 deposited with the ATCC under accession number PTA-1074. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo30_1 deposited with the ATCC under accession number PTA-1074. In further preferred embodiments, the present invention provides a polynucleotide 30 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 131 to amino acid 140 of SEQ ID NO:58.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
5 ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:57, but excluding the poly(A) tail at the
3' end of SEQ ID NO:57; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
15 vo30_1 deposited with the ATCC under accession number PTA-1074;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the
20 probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:57, but excluding the poly(A) tail at the
3' end of SEQ ID NO:57; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
30 vo30_1 deposited with the ATCC under accession number PTA-1074;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 48 to nucleotide
10 866, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 48 to nucleotide 866, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 48 to nucleotide 866. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:57 from nucleotide 114 to nucleotide 866, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 114 to nucleotide 866, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 114 to nucleotide 866.

In other embodiments, the present invention provides a composition comprising a
20 protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;
- (b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vo30_1 deposited with the ATCC under accession number PTA-1074;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 131 to amino acid 140 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 235 to nucleotide 510;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:59 from nucleotide 316 to nucleotide 510;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp25_1 deposited with the ATCC under accession number PTA-1074;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vp25_1 deposited with the ATCC under accession number PTA-1074;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp25_1 deposited with the ATCC under accession number PTA-1074;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp25_1 deposited with the ATCC under accession number PTA-1074;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- 25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:59.

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 235 to nucleotide 510; the nucleotide sequence of SEQ ID NO:59 from nucleotide 316 to nucleotide 510; the nucleotide sequence of the full-length protein coding sequence of clone vp25_1 deposited with the ATCC under accession number PTA-1074; or the nucleotide sequence of a mature protein coding sequence of clone vp25_1 deposited with the ATCC under accession number PTA-1074. In other preferred
10 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp25_1 deposited with the ATCC under accession number PTA-1074. In further preferred embodiments, the present invention provides a polynucleotide
15 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid
20 sequence from amino acid 41 to amino acid 50 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 25 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:59, but excluding the poly(A) tail at the
30 3' end of SEQ ID NO:59; and

- (ab) the nucleotide sequence of the cDNA insert of clone vp25_1 deposited with the ATCC under accession number PTA-1074;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize
- 10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 vp25_1 deposited with the ATCC under accession number PTA-1074;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 20 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but

25 excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 235 to nucleotide 510, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 235 to nucleotide 510, to a nucleotide

30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 235 to nucleotide 510. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:59 from nucleotide 316 to nucleotide 510, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 316 to nucleotide 510, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 316 to nucleotide 510.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
- (b) a fragment of the amino acid sequence of SEQ ID NO:60, the
10 fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
vp25_1 deposited with the ATCC under accession number PTA-1074;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ
ID NO:60 having biological activity, the fragment comprising the amino acid sequence
20 from amino acid 41 to amino acid 50 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:61;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:61 from nucleotide 177 to nucleotide 1626;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:61 from nucleotide 219 to nucleotide 1626;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-
length protein coding sequence of clone vq25_1 deposited with the ATCC under
accession number PTA-1074;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq25_1 deposited with the ATCC under accession number PTA-1074;
- 5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq25_1 deposited with the ATCC under accession number PTA-1074;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq25_1 deposited with the ATCC under accession number PTA-1074;
- 10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:62;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;
- 15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 177 to nucleotide 1626; the nucleotide sequence of SEQ ID NO:61 from nucleotide 219 to nucleotide 1626; the nucleotide sequence of the full-length protein coding sequence of clone vq25_1 deposited with the ATCC under accession number PTA-1074; or the nucleotide sequence of a mature protein coding sequence of clone vq25_1 deposited with the ATCC under accession number PTA-1074. In other preferred

30 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq25_1 deposited with the ATCC under accession number PTA-1074. In further preferred embodiments, the present invention provides a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
5 SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 236 to amino acid 245 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

Further embodiments of the invention provide isolated polynucleotides produced
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone vq25_1 deposited with the ATCC under accession number PTA-1074;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

- (bb) the nucleotide sequence of the cDNA insert of clone vq25_1 deposited with the ATCC under accession number PTA-1074;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 177 to nucleotide 1626, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 177 to nucleotide 1626, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 177 to nucleotide 1626. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 219 to nucleotide 1626, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 219 to nucleotide 1626, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 219 to nucleotide 1626.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:62;
- (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vq25_1 deposited with the ATCC under accession number PTA-1074;
- 30 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 236 to amino acid 245 of SEQ ID NO:62.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

DETAILED DESCRIPTION

ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone "vb24_1"

A polynucleotide of the present invention has been identified as clone "vb24_1". vb24_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb24_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb24_1 protein").

The nucleotide sequence of vb24_1 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 3 to 15 of SEQ ID NO:2 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb24_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb24_1 should be approximately 6033 bp.

The nucleotide sequence disclosed herein for vb24_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb24_1 demonstrated at least some similarity with sequences identified as AB005299 (Homo sapiens BAI 3 mRNA, complete cds), AB011122 (Homo sapiens mRNA for KIAA0550 protein, complete cds), N50991 (yy94e07.s1 Homo sapiens cDNA clone 281220 3'), and Q77404 (Human genome fragment (Preferred); standard; DNA). The predicted amino acid sequence disclosed herein for vb24_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vb24_1 protein demonstrated at least some similarity to sequences identified as AB005299 (BAI 3 [Homo sapiens]) and W37412 (Human G-protein coupled receptor HIBCD07). Based upon sequence similarity, vb24_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts eight potential transmembrane domains within the vb24_1 protein sequence, centered around amino acids 16, 888, 923, 952, 993, 1030, 1100, and 1138 of SEQ ID NO:2, respectively. The vb24_1 protein shares significant amino acid sequence similarity with GenBank Accession Number AB005299 (BAI 3 [Homo sapiens]), which is a splice variant of GenBank Accession Number AB011122 (KIAA0550 protein [Homo sapiens]), and shares amino acid similarity with other members of the BAI/secretin protein families. The members of the BAI/secretin protein families are G-protein-coupled receptors. The TopPredII profiles for some members of the BAI/secretin protein families are strikingly similar to that of vb24_1, with one transmembrane domain predicted at the N-terminus (approximately within the first 20 amino acids) and multiple transmembrane domains near the C-terminus. The N-terminal transmembrane domains of the BAI/secretin protein family members are described as leader/signal sequences, consistent with the first transmembrane domain in the predicted vb24_1 protein being a leader/signal sequence.

Clone "vc64_1"

A polynucleotide of the present invention has been identified as clone "vc64_1". vc64_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc64_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc64_1 protein").

The nucleotide sequence of vc64_1 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc64_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino acids 20 to 32 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 33. Due to the hydrophobic nature of the predicted leader/signal sequence, the TopPredII computer program predicts that is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc64_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc64_1 should be approximately 2022 bp.

The nucleotide sequence disclosed herein for vc64_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc64_1 demonstrated at least some similarity with sequences identified as AI217133 (qf47c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753170 3', mRNA sequence), T19353 (Human gene signature HUMGS00377; standard; cDNA to mRNA), and Z49239 (A.thaliana mRNA for putative dTDP-glucose 4-6-dehydratases). The predicted amino acid sequence disclosed herein for vc64_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc64_1 protein demonstrated at least some similarity to sequences identified as R98529 (dTDP-glucose dehydratase encoded by the acbB gene), U40800 (similar to thymidine diphosphoglucose 4,6-dehydratase [Caenorhabditis elegans]), and the dehydratases of many disparate species. The hydratase protein family is very diverse with proteins ranging in length from less than 300 to more than 400 amino acids. The vc64_1 protein appears to be an alternatively spliced variant of certain hydratases, and the existence of splice variants is also consistent with the diversity of the hydratase family. Based upon sequence similarity, vc64_1 proteins and each similar protein or peptide may share at least some activity.

vc64_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 5 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "vp20_1"

A polynucleotide of the present invention has been identified as clone "vp20_1". vp20_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp20_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp20_1 protein").

The nucleotide sequence of vp20_1 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp20_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6. Amino acids 34 to 46 of SEQ ID NO:6 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp20_1 protein.

Another potential vp20_1 reading frame and predicted amino acid sequence is encoded by basepairs 910 to 1293 of SEQ ID NO:5 and is reported as SEQ ID NO:88. Amino acids 9 to 21 of SEQ ID NO:88 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:88.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp20_1 should be approximately 1916 bp.

The nucleotide sequence disclosed herein for vp20_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp20_1 demonstrated at least some similarity with sequences identified as AA044732 (zk67e09.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 487912 3', mRNA sequence) and AA044769 (zk67e09.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 487912 5', mRNA sequence). Based upon sequence similarity, vp20_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the vp20_1 protein sequence, one centered around amino

acid 60 and another around amino acid 87 of SEQ ID NO:6. The TopPredII computer program also predicts one additional potential transmembrane domain within the protein of SEQ ID NO:88, centered around amino acid 80 of SEQ ID NO:88. The nucleotide sequence of the vp20_1 clone indicates that it may contain one or more MIR repeat sequences.

Clone "vq4_1"

A polynucleotide of the present invention has been identified as clone "vq4_1". vq4_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq4_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq4_1 protein").

The nucleotide sequence of vq4_1 as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq4_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8. Amino acids 7 to 19 of SEQ ID NO:8 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq4_1 protein.

Were the 'G' residue at position 336 of SEQ ID NO:7 to be deleted, two alternative overlapping vq4_1 reading frames and predicted amino acid sequences would result: the first alternative amino acid sequence is encoded by SEQ ID NO:7 from nucleotide 129 to what would then be nucleotide 359, and is reported in SEQ ID NO:89; the second alternative amino acid sequence is encoded by SEQ ID NO:7 from nucleotide 275 to what would then be nucleotide 730, and is reported in SEQ ID NO:90.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq4_1 should be approximately 831 bp.

The nucleotide sequence disclosed herein for vq4_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq4_1 demonstrated at least some similarity with sequences identified as M75099 (Human rapamycin- and FK506-binding protein, complete cds),

N36303 (yx99e09.r1 Homo sapiens cDNA clone 269896 5' similar to SW:FKB3_MOUSE P45878 FK506-BINDING PROTEIN PRECURSOR), and T18037 (Human FKBP-13 immunophilin cDNA; standard; cDNA). The predicted amino acid sequence disclosed herein for vq4_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq4_1 protein demonstrated at least some similarity to sequences identified as M75099 (rapamycin- and FK506-binding protein [Homo sapiens]) and R28980 (hRFKBP). Based upon sequence similarity, vq4_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vq4_1 protein sequence, one centered around amino acid 14 and another around amino acid 164 of SEQ ID NO:8.

Clone "vo7_1"

A polynucleotide of the present invention has been identified as clone "vo7_1". vo7_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo7_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo7_1 protein").

The nucleotide sequence of vo7_1 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo7_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino acids 14 to 26 of SEQ ID NO:10 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo7_1 protein.

If a nucleotide were added to the nucleotide sequence of SEQ ID NO:9 between residue 477 and residue 484, and if a purine residue were added to the nucleotide sequence of SEQ ID NO:9 between residue 896 and residue 900, another potential vo7_1 reading frame and predicted amino acid sequence encoded by what would then be basepairs 143 to 1336 of SEQ ID NO:9 is reported in SEQ ID NO:91. Amino acids 14 to 26 of SEQ ID NO:91 are a predicted leader/signal sequence, with the predicted mature amino acid

sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:91.

- 5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo7_1 should be approximately 1740 bp.

The nucleotide sequence disclosed herein for vo7_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo7_1 demonstrated at least some similarity with sequences
10 identified as L04733 (Homo sapiens kinesin light chain mRNA, complete cds) and W07481 (za96d09.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 300401 5' similar to gb L04733 KINESIN LIGHT CHAIN (HUMAN); mRNA sequence). The predicted amino acid sequence disclosed herein for vo7_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.
15 The predicted vo7_1 protein demonstrated at least some similarity to sequences identified as L04733 (kinesin light chain [Homo sapiens]). Movement of membrane-bounded organelles to intracellular destinations requires properly oriented microtubules and force-generating enzymes, such as the microtubule-stimulated ATPase kinesin. (See Cyr *et al.*, 1991, *Proc. Natl. Acad. Sci. USA* 88(22): 10114-10118, which is incorporated by
20 reference herein). Based upon sequence similarity, vo7_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vc65_1"

A polynucleotide of the present invention has been identified as clone "vc65_1".
25 vc65_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc65_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc65_1 protein").

The nucleotide sequence of vc65_1 as presently determined is reported in SEQ ID
30 NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc65_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12. Amino acids 14 to 26

of SEQ ID NO:12 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc65_1 protein.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc65_1 should be approximately 826 bp.

 The nucleotide sequence disclosed herein for vc65_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc65_1 demonstrated at least some similarity with sequences
10 identified as AA506313 (nh45c03.s1 NCI_CGAP_Pr5 Homo sapiens cDNA clone IMAGE:955300 similar to TR:G685170 G685170 ADHERIN; mRNA sequence) and T22080 (Human gene signature HUMGS03624). Based upon sequence similarity, vc65_1 proteins and each similar protein or peptide may share at least some activity.

15 Clone "vc66_1"

 A polynucleotide of the present invention has been identified as clone "vc66_1". vc66_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc66_1 is a full-length clone, including the entire coding
20 sequence of a secreted protein (also referred to herein as "vc66_1 protein").

 The nucleotide sequence of vc66_1 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc66_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 28 to 40
25 of SEQ ID NO:14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc66_1 protein.

 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
30 vc66_1 should be approximately 1652 bp.

 The nucleotide sequence disclosed herein for vc66_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. vc66_1 demonstrated at least some similarity with sequences identified as AA291293 (zs18d11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 685557 3', mRNA sequence). Based upon sequence similarity, vc66_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide
5 sequence of vc66_1 indicates that it may contain a LiMA5 repeat region.

Clone "vc68_1"

A polynucleotide of the present invention has been identified as clone "vc68_1". vc68_1 was isolated from a human fetal brain cDNA library and was identified as encoding
10 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc68_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc68_1 protein").

The nucleotide sequence of vc68_1 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the vc68_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16. Amino acids 15 to 27 of SEQ ID NO:16 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted
20 leader/signal sequence not be separated from the remainder of the vc68_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc68_1 should be approximately 2652 bp.

The nucleotide sequence disclosed herein for vc68_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. vc68_1 demonstrated at least some similarity with sequences identified as A1147732 (qb47e06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE 1703266 3' similar to WP F55C5.2 CE11152 GLYCEROPHOSPHORYLDIESTERPHOSPHODIESTERASELIKE; mRNA sequence), AC003108 (Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence),
30 and T26462 (Human gene signature HUMGS08704). The predicted amino acid sequence disclosed herein for vc68_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc68_1 protein

demonstrated at least some similarity to sequences identified as AC00310 (Unknown gene product [Homo sapiens]) and W89783 (Staphylococcus aureus protein SEQ ID #5231). Based upon sequence similarity, vc68_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional
5 potential transmembrane domain within the vc68_1 protein sequence centered around amino acid 38 of SEQ ID NO:16. The nucleotide sequence of vc68_1 indicates that it may contain an Alu repetitive element.

Clone "vk6_1"

10 A polynucleotide of the present invention has been identified as clone "vk6_1". vk6_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vk6_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vk6_1 protein").

15 The nucleotide sequence of vk6_1 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vk6_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 10 to 22 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted mature amino
20 acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vk6_1 protein.

If nine nucleotides encoding the amino acid sequence Met-Ile-Phe were inserted between nucleotide 678 and nucleotide 679 of SEQ ID NO:17, another potential vk6_1
25 reading frame and predicted amino acid sequence, encoded by what would then be basepairs 79 to 2427 of SEQ ID NO:17, is reported in SEQ ID NO:92.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vk6_1 should be approximately 4899 bp.

The nucleotide sequence disclosed herein for vk6_1 was searched against the
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vk6_1 demonstrated at least some similarity with sequences identified as AC006208 (Homo sapiens 3p21.1-9 PAC RPCI4-793P23 (Roswell Park

Cancer Institute Human PAC Library) complete sequence), AI127070 (qb97e10.x1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE 1708074 3', mRNA sequence), U28369 (Homo sapiens semaphorin V mRNA, complete cds), and V35367 (Human semaphorin encoding cDNA). The predicted amino acid sequence disclosed herein for vk6_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vk6_1 protein demonstrated at least some similarity to sequences identified as U28369 (semaphorin V [Homo sapiens]) and W63748 (Human semaphorin). The vk6_1 amino acid sequence also demonstrated significant similarities to the semaphorin and collapsin proteins of many species. "The semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules." (Kolodkin et al., 1993, *Cell* 75(7): 1389-99, which is incorporated by reference herein). Based upon sequence similarity, vk6_1 proteins and each similar protein or peptide may share at least some activity. Motif analysis detects an ATP/GTP-binding site motif A (P-loop) around residue 747 of SEQ ID NO:18. The TopPredII computer program predicts two additional potential transmembrane domains within the vk6_1 protein sequence, one centered around amino acid 140 and another around amino acid 336 of SEQ ID NO:18.

Clone "vo4_1"

A polynucleotide of the present invention has been identified as clone "vo4_1". vo4_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo4_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo4_1 protein").

The nucleotide sequence of vo4_1 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo4_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20. Amino acids 11 to 23 of SEQ ID NO:20 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo4_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo4_1 should be approximately 2383 bp.

The nucleotide sequence disclosed herein for vo4_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo4_1 demonstrated at least some similarity with sequences identified as AA613523 (nq22d01.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144609, mRNA sequence), E12646 (cDNA encoding cell growth inhibiting factor), and Q60729 (Human brain Expressed Sequence Tag EST00852). The predicted amino acid sequence disclosed herein for vo4_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo4_1 protein demonstrated at least some similarity to sequences identified as W74956 (Human secreted protein encoded by gene 77 clone HOEAS24) and Z92825 (C13C4.5 [Caeno-rhabditis elegans]). Based upon sequence similarity, vo4_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the vo4_1 protein sequence, centered around amino acids 69, 114, 169, and 207 of SEQ ID NO:20, respectively.

Clone "vo8_1"

A polynucleotide of the present invention has been identified as clone "vo8_1". vo8_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo8_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo8_1 protein").

The nucleotide sequence of vo8_1 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo8_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 10 to 22 of SEQ ID NO:22 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo8_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo8_1 should be approximately 3243 bp.

The nucleotide sequence disclosed herein for vo8_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
5 FASTA search protocols. vo8_1 demonstrated at least some similarity with sequences identified as AF007138 (Homo sapiens clone 23631 mRNA sequence), AI204925 (an02a08.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE 1684406 3' similar to TR Q92597 Q92597 RTP, COMPLETE CDS; mRNA sequence), and Q59200 (Human brain Expressed Sequence Tag EST00134). The predicted amino acid sequence
10 disclosed herein for vo8_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo8_1 protein demonstrated at least some similarity to sequences identified as AF045564 (development-related protein [Rattus norvegicus]). Based upon sequence similarity, vo8_1 proteins and each similar protein or peptide may share at least some activity.

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Clone "vo10_1"

A polynucleotide of the present invention has been identified as clone "vo10_1". vo10_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the
20 amino acid sequence of the encoded protein. vo10_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo10_1 protein").

The nucleotide sequence of vo10_1 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo10_1 protein corresponding
25 to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino acids 15 to 27 of SEQ ID NO:24 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo10_1 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo10_1 should be approximately 1048 bp.

The nucleotide sequence disclosed herein for vo10_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo10_1 demonstrated at least some similarity with sequences identified as AI193090 (qe69e08.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744262 3' similar to WP:F45G2.10 CE16053; mRNA sequence) and T19307 (Human gene signature HUMGS00329). The predicted amino acid sequence disclosed herein for vo10_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo10_1 protein demonstrated at least some similarity to sequences identified as Z93382 (F45G2.10 [Caenorhabditis elegans]). Based upon sequence similarity, vo10_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo20_1"

A polynucleotide of the present invention has been identified as clone "vo20_1". vo20_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo20_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo20_1 protein").

The nucleotide sequence of vo20_1 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo20_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Amino acids 6 to 18 of SEQ ID NO:26 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo20_1 protein.

If a nucleotide residue was deleted from the sequence beginning at nucleotide 770 and ending at nucleotide 774 of SEQ ID NO:25, another potential vo20_1 reading frame and predicted amino acid sequence, encoded by what would then be basepairs 102 to 932 of SEQ ID NO:25, is reported in SEQ ID NO:93.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo20_1 should be approximately 2067 bp.

The nucleotide sequence disclosed herein for vo20_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo20_1 demonstrated at least some similarity with sequences identified as AA452380 (zx29b11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 787869 5', mRNA sequence), L13291 Human ADP-ribosylarginine hydrolase mRNA, complete cds), and V05140 (cDNA encoding human ADP-ribosylarginine hydrolase). The predicted amino acid sequence disclosed herein for vo20_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo20_1 protein demonstrated at least some similarity to sequences identified as L13291 (ADP-ribosylarginine hydrolase [Homo sapiens]) and W46493 (Human ADP-ribosylarginine hydrolase). Based upon sequence similarity, vo20_1 proteins and each similar protein or peptide may share at least some activity. The predicted vo20_1 protein demonstrated at least some similarity to ADP-ribosylarginine hydrolases from other species as well, which catalyze the reverse reaction of mono-ADP-ribosylation. "ADP-ribosylarginine hydrolases specifically cleave the alpha-anomer, leading to release of ADP-ribose and regeneration of the free guanidino group of arginine" (Moss *et al.*, 1997, *Adv. Exp. Med. Biol.* 419: 25-33, which is incorporated by reference herein). Moss *et al.* also report that there might be a cell surface version of the hydrolase. The TopPredII computer program predicts two additional potential transmembrane domains within the vo20_1 protein sequence, one centered around amino acid 176 and another around amino acid 314 of SEQ ID NO:26.

Clone "vo21_1"

A polynucleotide of the present invention has been identified as clone "vo21_1". vo21_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo21_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo21_1 protein").

The nucleotide sequence of vo21_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo21_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28. Amino acids 18 to 30

of SEQ ID NO:28 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo21_1 protein.

- 5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo21_1 should be approximately 2560 bp.

 The nucleotide sequence disclosed herein for vo21_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant sequence similarities were identified. Motif
10 analysis revealed a cytochrome C motif around residue 3 of SEQ ID NO:28. The TopPredII computer program predicts an additional potential transmembrane domain within the vo21_1 protein sequence centered around amino acid 193 of SEQ ID NO:28. The nucleotide sequence of vo21_1 indicates that it may contain an Alu repetitive element.

15 Clone "vp24_1"

 A polynucleotide of the present invention has been identified as clone "vp24_1". vp24_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp24_1 is a full-length clone, including the
20 entire coding sequence of a secreted protein (also referred to herein as "vp24_1 protein").

 The nucleotide sequence of vp24_1 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 7 to 19
25 of SEQ ID NO:30 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp24_1 protein.

- The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
30 vp24_1 should be approximately 1536 bp.

 The nucleotide sequence disclosed herein for vp24_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. vp24_1 demonstrated at least some similarity with sequences identified as AA947280 (ok20a12.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE 1508350 3', mRNA sequence). Based upon sequence similarity, vp24_1 proteins and each similar protein or peptide may share at least some activity. The
5 TopPredII computer program predicts an additional potential transmembrane domain within the vp24_1 protein sequence centered around amino acid 55 of SEQ ID NO:30.

Clone "vo17_1"

A polynucleotide of the present invention has been identified as clone "vo17_1".
10 vo17_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo17_1 is a full-length clone, including the entire coding sequence of a protein (also referred to herein as "vo17_1 protein").

The nucleotide sequence of vo17_1 as presently determined is reported in SEQ ID
15 NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo17_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino acids 21 to 33 of SEQ ID NO:32 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 34.

20 Another potential vo17_1 reading frame and predicted amino acid sequence, encoded by basepairs 2530 to 2691 of SEQ ID NO:31, is reported in SEQ ID NO:94. Amino acids 2 to 14 of SEQ ID NO:94 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain
25 should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:94.

Another potential vo17_1 reading frame and predicted amino acid sequence, encoded by basepairs 402 to 785 of SEQ ID NO:31, is reported in SEQ ID NO:95. Amino acids 32 to 44 of SEQ ID NO:95 are a possible leader/signal sequence, with the predicted
30 mature amino acid sequence beginning at amino acid 45. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain

should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:95.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo17_1 should be approximately 2755 bp.

5 The nucleotide sequence disclosed herein for vo17_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo17_1 demonstrated at least some similarity with sequences identified as AF020762 (Homo sapiens clone 1400 unknown protein mRNA, partial cds), N91173 (zb12c08.s1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 301838 3',
10 mRNA sequence), and Q60597 (Human brain Expressed Sequence Tag EST02608). The predicted amino acid sequence disclosed herein for vo17_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo17_1 protein demonstrated at least some similarity to sequences identified as AF020762 (unknown protein [Homo sapiens]) and AF022770 (peripheral
15 benzodiazepine receptor associated protein [Mus musculus]). Benzodiazepine receptors are responsible for the manifestation of peripheral-type benzodiazepine recognition sites and are most likely to comprise binding domains for benzodiazepines and isoquinoline carboxamides. These integral membrane protein receptors play a role in the transport of porphyrins and heme and have a mitochondrial subcellular localization. Based upon
20 sequence similarity, vo17_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vq11_1"

A polynucleotide of the present invention has been identified as clone "vq11_1".
25 vq11_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq11_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq11_1 protein").

The nucleotide sequence of vq11_1 as presently determined is reported in SEQ ID
30 NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq11_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Amino acids 15 to 27

of SEQ ID NO:34 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq11_1 protein.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq11_1 should be approximately 1177 bp.

 The nucleotide sequence disclosed herein for vq11_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq11_1 demonstrated at least some similarity with sequences
10 identified as R39062 (yd08g11.s1 Homo sapiens cDNA clone 25117 3'). Based upon sequence similarity, vq11_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vq12_1"

15 A polynucleotide of the present invention has been identified as clone "vq12_1". vq12_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq12_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq12_1 protein").

20 The nucleotide sequence of vq12_1 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq12_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36. Amino acids 2 to 14 of SEQ ID NO:36 are a predicted leader/signal sequence, with the predicted mature amino
25 acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq12_1 protein.

 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq12_1 should be approximately 1435 bp.

30 The nucleotide sequence disclosed herein for vq12_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq12_1 demonstrated at least some similarity with sequences

identified as AI479299 (tm56h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2162161 3', mRNA sequence). Based upon sequence similarity, vq12_1 proteins and each similar protein or peptide may share at least some activity. Motifs analysis detects a glycoprotein hormones beta chain signature centered approximately around amino acid 192 of SEQ ID NO:36.

Clone "vq14_1"

A polynucleotide of the present invention has been identified as clone "vq14_1". vq14_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq14_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq14_1 protein").

The nucleotide sequence of vq14_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq14_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Amino acids 3 to 15 of SEQ ID NO:38 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq14_1 protein.

If two nucleotides were inserted between nucleotide 651 and nucleotide 657 of SEQ ID NO:37, another potential vq14_1 reading frame and predicted amino acid sequence, encoded by what would then be basepairs 32 to 712 of SEQ ID NO:37, is reported in SEQ ID NO:96. Amino acids 3 to 15 of SEQ ID NO:96 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:96.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq14_1 should be approximately 1183 bp.

The nucleotide sequence disclosed herein for vq14_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. vq14_1 demonstrated at least some similarity with sequences identified as AI291113 (qm10d12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881431 3' similar to contains LTR1.t3 TAR1 repetitive element; mRNA sequence) and T80413 (Tylactone synthase gene cluster). Based upon sequence similarity, vq14_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts 7 additional potential transmembrane domains within the vq14_1 protein sequence, centered around amino acids 59, 108, 137, 176, 220, 240, and 250 of SEQ ID NO:38, respectively. The protein of SEQ ID NO:96 is also predicted to have 4 additional potential transmembrane domains, centered around amino acids 59, 108, 137, and 176 of SEQ ID NO:96, respectively.

Clone "vq15_1"

A polynucleotide of the present invention has been identified as clone "vq15_1". vq15_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq15_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq15_1 protein").

The nucleotide sequence of vq15_1 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq15_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40. Amino acids 74 to 86 of SEQ ID NO:40 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 87. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq15_1 protein.

Another potential vq15_1 reading frame and predicted amino acid sequence, encoded by basepairs 18 to 353 of SEQ ID NO:39, is reported in SEQ ID NO:97. Amino acids 24 to 36 of SEQ ID NO:97 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 37. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:97.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq15_1 should be approximately 1519 bp.

The nucleotide sequence disclosed herein for vq15_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq15_1 demonstrated at least some similarity with sequences identified as AA573785 (nk07e12.s1 NCI_CGAP_Co2 Homo sapiens cDNA clone IMAGE 1012846, mRNA sequence), AF115384 (Homo sapiens LR8 (LR8) mRNA, complete cds), and T20820 (Human gene signature HUMGS02069). The predicted amino acid sequence disclosed herein for vq15_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq15_1 protein demonstrated at least some similarity to sequences identified as AF11538 (LR8 [Homo sapiens]) and W75125 (Human secreted protein encoded by gene 69 clone HPEBD70). LR8 is a protein of unknown function, "expressed by a subpopulation of human lung fibroblasts by differential display" (Lurton *et al.*, 1999, *Am J Respir Cell Mol Biol* 20(2): 327-31, which is incorporated by reference herein). Based upon sequence similarity, vq15_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the vq15_1 protein sequence, one centered around amino acid 138 and another around amino acid 218 of SEQ ID NO:40.

20

Clone "vq17_1"

A polynucleotide of the present invention has been identified as clone "vq17_1". vq17_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq17_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq17_1 protein").

The nucleotide sequence of vq17_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq17_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 7 to 19 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted

leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq17_1 protein.

Another potential vq17_1 reading frame and predicted amino acid sequence, encoded by basepairs 1947 to 2342 of SEQ ID NO:41, is reported in SEQ ID NO:98.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq17_1 should be approximately 2869 bp.

The nucleotide sequence disclosed herein for vq17_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq17_1 demonstrated at least some similarity with sequences
10 identified as AA225412 (nc24f07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1009093, mRNA sequence) and T20503 (Human gene signature HUMGS01709). Based upon sequence similarity, vq17_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vq17_1 protein sequence centered around
15 amino acid 65 of SEQ ID NO:42. The TopPredII computer program predicts two potential transmembrane domains within the protein sequence of SEQ ID NO:98, one centered around amino acid 66 and another around amino acid 79 of SEQ ID NO:98.

Clone "vq18_1"

20 A polynucleotide of the present invention has been identified as clone "vq18_1". vq18_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq18_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq18_1 protein").

25 The nucleotide sequence of vq18_1 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq18_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44. Amino acids 11 to 23 of SEQ ID NO:44 are a predicted leader/signal sequence, with the predicted mature amino
30 acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq18_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq18_1 should be approximately 687 bp.

The nucleotide sequence disclosed herein for vq18_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq18_1 demonstrated at least some similarity with sequences identified as R47882 (yj62d11.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE 153333 5', mRNA sequence). Based upon sequence similarity, vq18_1 proteins and each similar protein or peptide may share at least some activity. The vq18_1 protein appears to be one member of a family of proteins produced by alternative splicing (see, for example, the yd51_1 protein of International Application No. PCT/US99/10843, which is incorporated by reference herein).

Clone "vq22_1"

A polynucleotide of the present invention has been identified as clone "vq22_1". vq22_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq22_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq22_1 protein").

The nucleotide sequence of vq22_1 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq22_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 16 to 28 of SEQ ID NO:46 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 29. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq22_1 protein.

If the following changes were made to the nucleotide sequence of SEQ ID NO:45 — deletion of nucleotides 1096 and 1097; deletion of one nucleotide from the group of nucleotides 1142, 1143, and 1144; deletion of one nucleotide from the group of nucleotides 1159, 1160, and 1161; deletion of one nucleotide from the group of nucleotides 1187, 1188, and 1189; and insertion of a "G" residue between nucleotide 1204 and nucleotide 1207 — another potential reading frame would be created from what would then be nucleotides 65

to1327, with a predicted amino acid sequence reported as SEQ ID NO:99. Amino acids 16 to 28 of SEQ ID NO:99 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 29. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain
5 should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:99.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq22_1 should be approximately 1653 bp.

The nucleotide sequence disclosed herein for vq22_1 was searched against the
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq22_1 demonstrated at least some similarity with sequences identified as AA716162 (zg63f01.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:398041 3', mRNA sequence) and T26470 (Human gene signature HUMGS08712). The predicted amino acid sequence disclosed herein for vq22_1 was
15 searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq22_1 protein demonstrated at least some similarity to sequences identified as U58748 (similar to potential transmembrane domains in *S. cerevisiae* nuclear division RFT1 protein (SP P38206) [*Caenorhabditis elegans*]). Based upon sequence similarity, vq22_1 proteins and each similar protein or peptide may
20 share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within both the vq22_1 protein sequence and the amino acid sequence of the protein of SEQ ID NO:99, centered around amino acids 96, 126, 181, and 343, respectively, of SEQ ID NO:46 and of SEQ ID NO:99.

25 Clone "vr3_1"

A polynucleotide of the present invention has been identified as clone "vr3_1". vr3_1 was isolated from a human adult muscle cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vr3_1 is a full-length clone, including the
30 entire coding sequence of a secreted protein (also referred to herein as "vr3_1 protein").

The nucleotide sequence of vr3_1 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the vr3_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 2 to 14 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vr3_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vr3_1 should be approximately 3133 bp.

The nucleotide sequence disclosed herein for vr3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vr3_1 demonstrated at least some similarity with sequences identified as AI302099 (qn57g10.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE 1902402 3' similar to gb M14058 COMPLEMENT C1r COMPONENT PRECURSOR (HUMAN); mRNA sequence) and M14058 (Human complement C1r mRNA, complete cds). The predicted amino acid sequence disclosed herein for vr3_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vr3_1 protein demonstrated at least some similarity to sequences identified as M14058 (human complement C1r [Homo sapiens]). C1r is a zymogen of a serine protease that is involved in the activation of the first component of the classical pathway of the complement system (Leytus *et al.*, 1986, *Biochemistry* 25 (17): 4855-4863, which is incorporated by reference herein). Based upon sequence similarity, vr3_1 proteins and each similar protein or peptide may share at least some activity. Motifs analysis detects a serine proteases, trypsin family, active site around residue 407 of SEQ ID NO:48. Hidden Markov Model analysis detects a CUB domain from residue 16 to residue 137 of SEQ ID NO:48, and a trypsin profile from residue 222 to residue 456 of SEQ ID NO:48. The nucleotide sequence of vr3_1 indicates that it may contain an Alu repetitive element.

Clone "vb26_1"

A polynucleotide of the present invention has been identified as clone "vb26_1". vb26_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid

sequence of the encoded protein. vb26_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb26_1 protein").

The nucleotide sequence of vb26_1 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the vb26_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50. Amino acids 13 to 25 of SEQ ID NO:50 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted
10 leader/signal sequence not be separated from the remainder of the vb26_1 protein.

The nucleotide and amino acid sequences of vb26_1 are related to those of clone vc8_1, described in U.S. application Ser. No. 09/298,733. Clone vb26_1 contains the entire coding sequence of clone vc8_1, and has an additional three nucleotides at nucleotides 1283 to 1285 of SEQ ID NO:49.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb26_1 should be approximately 2974 bp.

The nucleotide sequence disclosed herein for vb26_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb26_1 demonstrated at least some similarity with sequences
20 identified as AI807015 (wf37b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357745 3' similar to SW:NDC1_RABIT Q28615 RENAL SODIUM/DICARBOXYLATE COTRANSPORTER; mRNA sequence), U26209 (Human renal sodium/dicarboxylate cotransporter (NADC1) mRNA, complete cds), and V27580 (Human hepatocyte nuclear factor 4 isoform gamma DNA). The predicted amino acid sequence
25 disclosed herein for vb26_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vb26_1 protein demonstrated at least some similarity to sequences identified as U87318 (NaDC-2 [Xenopus laevis]) and W98815 (H. pylori GHPO 1401 protein). Human renal sodium/dicarboxylate cotransporter (NADC1) displays remarkably wide substrate
30 selectivity, covering endogenous substrates such as cyclic nucleotides, a prostaglandin and uric acid, and a variety of drugs with different structures (e.g. antibiotics; a nonsteroidal anti-inflammatory drug, diuretics, an antineoplastic drug, and a uricosuric drug); this

protein is a multispecific organic anion transporter at the basolateral membrane of the proximal tubule (Sekine *et al.*, 1997, *J. Biol. Chem.* 272 (30): 18526-9, which is incorporated by reference herein). Based upon sequence similarity, vb26_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer
5 program predicts 11 probable transmembrane domains within the vb26_1 protein sequence, centered around amino acids 46, 61, 132, 282, 323, 385, 423, 508, 529, 556, and 598 of SEQ ID NO:50, respectively, and an additional two putative transmembrane domains centered around residues 91 and 472 of SEQ ID NO:50.

10 Clone "vc70_1"

A polynucleotide of the present invention has been identified as clone "vc70_1". vc70_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc70_1 is a full-length clone, including the entire coding
15 sequence of a secreted protein (also referred to herein as "vc70_1 protein").

The nucleotide sequence of vc70_1 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc70_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 15 to 27
20 of SEQ ID NO:52 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc70_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
25 vc70_1 should be approximately 2187 bp.

The nucleotide sequence disclosed herein for vc70_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc70_1 demonstrated at least some similarity with sequences identified as AI423223 (tf26f01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone
30 IMAGE:2097337 3', mRNA sequence) and X33812 (Coding sequence for human secreted protein cb96_10). The predicted amino acid sequence disclosed herein for vc70_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the

BLASTX search protocol. The predicted vc70_1 protein demonstrated at least some similarity to sequences identified as Y05319 (Human secreted protein cb96_10). Based upon sequence similarity, vc70_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts eight additional potential
5 transmembrane domains within the vc70_1 protein sequence, centered around amino acids 58, 110, 153, 204, 316, 373, 420, and 502 of SEQ ID NO:52, respectively. The vc70_1 protein appears to be a splice variant of the cb96_10 protein, with the vc70_1 protein having an additional 73 amino acids at the N-terminal end containing a signal sequence and an additional transmembrane domain.

10

Clone "vo28_1"

A polynucleotide of the present invention has been identified as clone "vo28_1". vo28_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of
15 the encoded protein. vo28_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "vo28_1 protein").

The nucleotide sequence of vo28_1 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo28_1 protein corresponding
20 to the foregoing nucleotide sequence is reported in SEQ ID NO:54.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo28_1 should be approximately 2056 bp.

The nucleotide sequence disclosed herein for vo28_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. vo28_1 demonstrated at least some similarity with sequences identified as F22780 (HSPD07683 HM3 Homo sapiens cDNA clone LL44/H10, mRNA sequence). Based upon sequence similarity, vo28_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vo28_1 indicates that it may contain an Alu repetitive element.

30

Clone "vo29_1"

A polynucleotide of the present invention has been identified as clone "vo29_1". vo29_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo29_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo29_1 protein").

The nucleotide sequence of vo29_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo29_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 8 to 20 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21; amino acids 5 to 17 of SEQ ID NO:56 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 18; and amino acids 11 to 23 of SEQ ID NO:56 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 24. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:56.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo29_1 should be approximately 1803 bp.

The nucleotide sequence disclosed herein for vo29_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo29_1 demonstrated at least some similarity with sequences identified as AI433801 (th81f07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125093 3' similar to SW:YMNO_YEAST Q03103 HYPOTHETICAL 65.0 KD PROTEIN IN COX14 5'REGION PRECURSOR; mRNA sequence), AR018794 (Sequence 76 from patent US 5783182), and X19751 (Mammalian Ero1 DNA). The predicted amino acid sequence disclosed herein for vo29_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo29_1 protein demonstrated at least some similarity to sequences identified as AC00577 (unknown protein [Arabidopsis thaliana]), W99801 (Mammalian Ero1 protein), and Y03632 (Hypoxia-regulated gene RTP241 product). Ero1 regulates the oxidation potential

of the endoplasmic reticulum, and may be used to increase disulfide bond formation in proteins during their production and/or purification. Based upon sequence similarity, vo29_1 proteins and each similar protein or peptide may share at least some activity. Motifs analysis detects an EF-hand calcium binding domain centered around amino acid
5 159 of SEQ ID NO:56.

Clone "vo30_1"

A polynucleotide of the present invention has been identified as clone "vo30_1". vo30_1 was isolated from a human adult pancreas cDNA library and was identified as
10 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo30_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo30_1 protein").

The nucleotide sequence of vo30_1 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the vo30_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58. Amino acids 10 to 22 of SEQ ID NO:58 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted
20 leader/signal sequence not be separated from the remainder of the vo30_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo30_1 should be approximately 1356 bp.

The nucleotide sequence disclosed herein for vo30_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. vo30_1 demonstrated at least some similarity with sequences identified as AA397685 (zt87d03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE 729317 5', mRNA sequence) and AI983410 (wu19c10.x1 Soares Dieckgraefe colon NHCD Homo sapiens cDNA clone IMAGE:990757 3' similar to contains TAR1.t3 TAR1 repetitive element; mRNA sequence). Based upon sequence similarity, vo30_1
30 proteins and each similar protein or peptide may share at least some activity. Motifs analysis detects an ATP/GTP binding site motif A (P-loop) centered around amino acid 38 of SEQ ID NO:58.

Clone "vp25_1"

A polynucleotide of the present invention has been identified as clone "vp25_1". vp25_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp25_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp25_1 protein").

The nucleotide sequence of vp25_1 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp25_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60. Amino acids 15 to 27 of SEQ ID NO:60 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp25_1 protein.

Another potential reading frame, encoded by nucleotides 1362 to 1622 of SEQ ID NO:59, is reported as the amino acid sequence of SEQ ID NO:100. Amino acids 5 to 17 of SEQ ID NO:100 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:100.

Another potential reading frame, encoded by nucleotides 2560 to 2820 of SEQ ID NO:59, is reported as the amino acid sequence of SEQ ID NO:101. Amino acids 21 to 33 of SEQ ID NO:101 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 34. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:101.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp25_1 should be approximately 2989 bp.

The nucleotide sequence disclosed herein for vp25_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. vp25_1 demonstrated at least some similarity with sequences identified as AA481107 (aa29d01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814657 5', mRNA sequence), AF146793 (Mus musculus protein B gene, partial cds; and CLOCK (Clock), PFT27 (pPFT27), and H5AR (H5AR) genes, complete cds),
5 AI081234 (oy67a03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE 1670860 3' similar to SW PF27_MOUSE P52875 TRANSMEMBRANE PROTEIN PFT27; contains MSR1.t1 MSR1 repetitive element), and X37441 (Human secreted protein cDNA fragment containing gene 55). The predicted amino acid sequence disclosed herein for vp25_1 was searched against the GenPept and GeneSeq amino acid sequence databases
10 using the BLASTX search protocol. The predicted vp25_1 protein demonstrated at least some similarity to sequences identified as AF14679 (PFT27 [Mus musculus]) and Y07843 (Human secreted protein fragment #2 encoded from gene 55). Based upon sequence similarity, vp25_1 proteins and each similar protein or peptide may share at least some activity. The vp25_1 protein and the proteins of database entries AF14679 and Y07843
15 appear to be members of a family of proteins produced as splice variants. The nucleotide sequence of vp25_1 indicates that it may contain an Alu repetitive element.

Clone "vq25_1"

A polynucleotide of the present invention has been identified as clone "vq25_1".
20 vq25_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq25_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq25_1 protein").

The nucleotide sequence of vq25_1 as presently determined is reported in SEQ ID
25 NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq25_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62. Amino acids 2 to 14 of SEQ ID NO:62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15; amino acids 4 to 16 of SEQ ID NO:62 are also
30 a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 17. Due to the hydrophobic nature of these predicted

leader/signal sequence, each is likely to act as a transmembrane domain should it not be separated from the remainder of the vq25_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq25_1 should be approximately 2048 bp.

5 The nucleotide sequence disclosed herein for vq25_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq25_1 demonstrated at least some similarity with sequences identified as AC007026 (Homo sapiens clone DJ0751G11, complete sequence), AI087294 (oz77h01.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE
10 1681393 3' similar to SW CTCF_HUMAN P49711 TRANSCRIPTIONAL REPRESSOR CTCF; mRNA sequence), AW003280 (wq64h08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2476095 3' similar to TR:Q60694 Q60694 RE1-SILENCING TRANSCRIPTION FACTOR; mRNA sequence), and X00648 (Human secreted protein gene 38 clone HODCV74). The predicted amino acid sequence disclosed herein for
15 vq25_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq25_1 protein demonstrated at least some similarity to sequences identified as AC00487 (zinc finger-like; similar to P52742 (PID g1731411) [Homo sapiens]) and R99364 (Human REST protein DNA binding domain). Based upon sequence similarity, vq25_1 proteins and each similar protein or
20 peptide may share at least some activity. Motifs analysis detects three Zinc-finger, C2H2-type, domains centered around amino acids 149, 359, and 387 of SEQ ID NO:62, respectively. Hidden markov model analysis detects eight of these Zinc-finger, C2H2-type, domains approximately at amino acids 91 to 113, 119 to 141, 147 to 169, 301 to 323, 329 to 351, 357 to 379, 385 to 407, and 413 to 435 of SEQ ID NO:62, respectively.

25

Deposit of Clones

Clones vb24_1, vc64_1, vp20_1, and vq4_1 were deposited on February 17, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty
30 and were given the accession number 207113, from which each clone comprising a particular polynucleotide is obtainable.

Clone vo7_1 was deposited on July 15, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number PTA-362, from which the vo7_1 clone comprising a particular polynucleotide is obtainable.

5 Clones vc65_1, vc66_1, vc68_1, vk6_1, vo4_1, vo8_1, vo10_1, vo20_1, vo21_1, and vp24_1 were deposited on July 15, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-361, from which each clone comprising a particular polynucleotide is obtainable.

10 Clone vo17_1 was deposited on July 15, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number PTA-366, from which the vo17_1 clone comprising a particular polynucleotide is obtainable.

15 Clones vq11_1, vq12_1, vq14_1, vq15_1, vq17_1, vq18_1, vq22_1, and vr3_1 were deposited on July 15, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-367, from which each clone comprising a particular polynucleotide is obtainable.

20 Clone vb26_1 was deposited on August 11, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number PTA-501. (Note that due to a typographical error, the deposit of clone vb26_1 under the accession number PTA-501 was initially recorded at the ATCC as a deposit of clone "YB26_1".)

25 Clones vc70_1, vo28_1, vo29_1, vo30_1, vp25_1, and vq25_1 were deposited on December 21, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-1074, from which each clone comprising a particular polynucleotide is obtainable.

30 All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in these composite deposits. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

	<u>Clone</u>	<u>Probe Sequence</u>
25	vb24_1	SEQ ID NO:63
	vc64_1	SEQ ID NO:64
	vp20_1	SEQ ID NO:65
	vq4_1	SEQ ID NO:66
	vo7_1	SEQ ID NO:67
30	vc65_1	SEQ ID NO:68
	vc66_1	SEQ ID NO:69
	vc68_1	SEQ ID NO:70

	vk6_1	SEQ ID NO:71
	vo4_1	SEQ ID NO:72
	vo8_1	SEQ ID NO:73
	vo10_1	SEQ ID NO:74
5	vo20_1	SEQ ID NO:75
	vo21_1	SEQ ID NO:76
	vp24_1	SEQ ID NO:77
	vo17_1	SEQ ID NO:78
	vq11_1	SEQ ID NO:79
10	vq12_1	SEQ ID NO:80
	vq14_1	SEQ ID NO:81
	vq15_1	SEQ ID NO:82
	vq17_1	SEQ ID NO:83
	vq18_1	SEQ ID NO:84
15	vq22_1	SEQ ID NO:85
	vr3_1	SEQ ID NO:86
	vb26_1	SEQ ID NO:87

In preferred probes/primers, the second nucleotide position is occupied by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

- 25 (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- (b) It should be designed to have a T_m of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with γ -³²P ATP (specific activity 6000 Ci/mmmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established

methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4×10^6 dpm/pmole.

5 The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 μ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 μ g/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid
10 bacteriological media containing L-broth containing ampicillin at 100 μ g/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

15 The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 μ g/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1×10^6 dpm/mL. The filter is then preferably
20 incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to
25 visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

30 Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as

described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding
5 sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

10 The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with the ATCC) in a suitable mammalian cell
15 or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are
20 derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed
25 herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

30 The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible

to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* **15**(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* **62**(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* **58**: 1-39; all of which are incorporated by reference herein). The desired change in gene expression can also be achieved through the use of double-stranded ribonucleotide molecules having some complementarity to the mRNA transcribed from the gene, and which interfere with the transcription, stability, or expression of the mRNA ("RNA interference" or "RNAi"; Fire *et al.*, 1998, *Nature* **391** (6669): 806-811; Montgomery *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* **95** (26): 15502-15507; and Sharp, 1999, *Genes Dev.* **13** (2): 139-141; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous

sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably

30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington
5 University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4,
which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish,
1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* 266: 460-480;
Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* 215:
403-410; Gish and States, 1993, Identification of protein coding regions by database
10 similarity search, *Nature Genetics* 3: 266-272; Karlin and Altschul, 1993, Applications and
statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci.*
USA 90: 5873-5877; all of which are incorporated by reference herein). WU-BLAST
version 2.0 executable programs for several UNIX platforms can be downloaded from
ftp://blast.wustl.edu/blast/executables. The complete suite of search programs (BLASTP,
15 BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to
several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or
redistributed in any form or manner without the express written consent of the author; but
the posted executables may otherwise be freely used for commercial, nonprofit, or
academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX,
20 TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database
search itself, and thus yield much better sensitivity and selectivity while producing the
more easily interpreted output. Gapping can optionally be turned off in all of these
programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins
and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including
25 zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty,
fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R)
is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any
integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven,
twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any
30 combination of values for Q and R can be used in order to align sequences so as to
maximize overlap and identity while minimizing sequence gaps. The default amino acid

comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* **22**: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* **3**:103-112; Johansson *et al.*, 1995, *Genomics* **25**: 682-690; Lyons *et al.*, 1997, *Nature Genetics* **15**: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* **13**(10): 393-399; Carver and Stubbs, 1997, *Genome Research* **7**:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60%

sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and
5 identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency
10 conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	<50	T _B *; 1xSSC	T _B *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	<50	T _D *; 1xSSC	T _D *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	RNA:RNA	<50	T _F *; 1xSSC	T _F *; 1xSSC
10	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	<50	T _H *; 4xSSC	T _H *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	<50	T _J *; 4xSSC	T _J *; 4xSSC
	K	RNA:RNA	≥ 50	70°C, 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	<50	T _L *; 2xSSC	T _L *; 2xSSC
15	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	<50	T _N *; 6xSSC	T _N *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	DNA:RNA	<50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	20	R	RNA:RNA	<50	T _R *; 4xSSC

[‡]: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

[†]: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log₁₀[Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable

bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope.

One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

10 The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis.
15 Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or
20 immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA
25 sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution,
30 replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the
5 present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited
10 herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular
20 stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers
25 for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes
30 a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi

et al., 1997, *Proc. Natl. Acad. Sci. USA* **94**: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to
5 determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue
10 differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or
15 small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning:
20 A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

25 Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid
30 preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors
5 discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G,
10 M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-
15 Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992;
20 Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: *Polyclonal T cell stimulation*, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and
25 *Measurement of mouse and human Interferon γ* , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: *Measurement of Human and Murine Interleukin 2 and Interleukin 4*, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and
30 Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al.,

- Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.
- 10 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience
- 15 (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

20

Immune Stimulating or Suppressing Activity

- A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies
- 25 and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral,
- 30 bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course,

in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a

monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune

disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide

having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

- 5 The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can
10 be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte
15 antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific
20 immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation,
25 those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986;
30 Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

- 5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

- 20 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

- 30 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991;

Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 5 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelosuppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without
5 limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described
10 in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In
15 *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*.
R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen,
T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179,
20 Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

25. A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in
30 circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open

fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

5 A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or
10 cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in
15 circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in
20 repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or
25 ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include
30 an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and

peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International

Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year 5 Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related 10 activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful 15 as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin 20 molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

25 Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

30 A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes,

fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in
5 treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell
10 population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by
15 the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion
20 include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al. Eur. J. Immunol. 25: 1744-1748; Gruber et al.
25 J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation
30 disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation

of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 5 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

10 Receptor/Ligand Activity

- A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors
15 involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.
- 20 A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- Suitable assays for receptor-ligand activity include without limitation those
25 described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.
30 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and

the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression
5 reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin
10 expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins,
15 restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately
20 expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a
25 polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer
30 patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. *J Biol Chem* 270 (32): 18809-18817, 1995; Miyaki et al. *Oncogene* 11: 2547-2552, 1995; Ozawa et al. *Cell* 63: 1033-1038, 1990.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins

including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin
5 and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically
10 acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as
15 disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient
20 to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in
25 the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination
30 with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either

simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic
5 factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous
10 administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or
15 an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain
20 physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

25 When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical
30 composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection,

Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition
5 of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses
10 of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 mg to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein of the present
15 invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the
20 range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the
25 term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein. Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

30 Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example,

Goding, 1983, Monoclonal antibodies: principles and practice, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in Current Protocols in Immunology, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, supra; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in Current Protocols in Immunology, Unit 2.8, Greene Publishing Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* 14: 845-851; Mendez *et al.*, 1997, *Nature Genetics* 15: 146-156 (erratum *Nature Genetics* 16: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl

cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress

can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a
5 mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells.
10 Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - (a) the nucleotide sequence of SEQ ID NO:1;
 - (b) the nucleotide sequence of SEQ ID NO:1 from nucleotide 737 to nucleotide 5302;
 - (c) the nucleotide sequence of SEQ ID NO:1 from nucleotide 782 to nucleotide 5302;
 - (d) the nucleotide sequence of the full-length protein coding sequence of clone vb24_1 deposited with the ATCC under accession number 361;
 - (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb24_1 deposited with the ATCC under accession number 361;
 - (f) the nucleotide sequence of a mature protein coding sequence of clone vb24_1 deposited with the ATCC under accession number 361;
 - (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb24_1 deposited with the ATCC under accession number 361;
 - (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
 - (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
 - (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
 - (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:1.

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.
3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:
 - (a) growing a culture of a host cell in a suitable culture medium, wherein the host cell has been transformed with the polynucleotide of claim 2; and
 - (b) purifying said protein from the culture.
6. A protein produced according to the process of claim 5.
7. An isolated polynucleotide encoding the protein of claim 6.
8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone vb24_1 deposited with the ATCC under accession number 361.
9. A protein comprising an amino acid sequence selected from the group consisting of:
 - (a) the amino acid sequence of SEQ ID NO:2;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vb24_1 deposited with the ATCC under accession number 361;the protein being substantially free from other mammalian proteins.
10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.

11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.

12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:3;
- (b) the nucleotide sequence of SEQ ID NO:3 from nucleotide 60 to nucleotide 1130;
- (c) the nucleotide sequence of SEQ ID NO:3 from nucleotide 156 to nucleotide 1130;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc64_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc64_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc64_1 deposited with the ATCC under accession number 361;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc64_1 deposited with the ATCC under accession number 361;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:3.

13. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vc64_1 deposited with the ATCC under accession number 361;
- the protein being substantially free from other mammalian proteins.

14. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:5;
- (b) the nucleotide sequence of SEQ ID NO:5 from nucleotide 195 to nucleotide 1298;
- (c) the nucleotide sequence of SEQ ID NO:5 from nucleotide 333 to nucleotide 1298;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp20_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp20_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp20_1 deposited with the ATCC under accession number 361;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp20_1 deposited with the ATCC under accession number 361;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:5.

15. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vp20_1 deposited with the ATCC under accession number 361;
- the protein being substantially free from other mammalian proteins.

16. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:7;
- (b) the nucleotide sequence of SEQ ID NO:7 from nucleotide 129 to nucleotide 731;
- (c) the nucleotide sequence of SEQ ID NO:7 from nucleotide 186 to nucleotide 731;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq4_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq4_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq4_1 deposited with the ATCC under accession number 361;

- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq4_1 deposited with the ATCC under accession number 361;
 - (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
 - (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;
 - (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
 - (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:7.
17. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:8;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq4_1 deposited with the ATCC under accession number 361;
- the protein being substantially free from other mammalian proteins.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:9;
 - (b) the nucleotide sequence of SEQ ID NO:9 from nucleotide 143 to nucleotide 571;
 - (c) the nucleotide sequence of SEQ ID NO:9 from nucleotide 221 to nucleotide 571;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo7_1 deposited with the ATCC under accession number 361;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo7_1 deposited with the ATCC under accession number 361;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo7_1 deposited with the ATCC under accession number 361;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo7_1 deposited with the ATCC under accession number 361;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:9.

19. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:10;

(b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo7_1 deposited with the ATCC under accession number 361;

the protein being substantially free from other mammalian proteins.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:11;
- (b) the nucleotide sequence of SEQ ID NO:11 from nucleotide 112 to nucleotide 570;
- (c) the nucleotide sequence of SEQ ID NO:11 from nucleotide 190 to nucleotide 570;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc65_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc65_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc65_1 deposited with the ATCC under accession number 361;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc65_1 deposited with the ATCC under accession number 361;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:11.

21. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vc65_1 deposited with the ATCC under accession number 361;
- the protein being substantially free from other mammalian proteins.

22. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:13;
- (b) the nucleotide sequence of SEQ ID NO:13 from nucleotide 4 to nucleotide 261;
- (c) the nucleotide sequence of SEQ ID NO:13 from nucleotide 124 to nucleotide 261;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc66_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc66_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc66_1 deposited with the ATCC under accession number 361;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc66_1 deposited with the ATCC under accession number 361;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:13.

23. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vc66_1 deposited with the ATCC under accession number 361;
- the protein being substantially free from other mammalian proteins.

24. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:15;
- (b) the nucleotide sequence of SEQ ID NO:15 from nucleotide 135 to nucleotide 1227;
- (c) the nucleotide sequence of SEQ ID NO:15 from nucleotide 216 to nucleotide 1227;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc68_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc68_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc68_1 deposited with the ATCC under accession number 361;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc68_1 deposited with the ATCC under accession number 361;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:15.

25. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc68_1 deposited with the ATCC under accession number 361;

the protein being substantially free from other mammalian proteins.

26. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:17;

(b) the nucleotide sequence of SEQ ID NO:17 from nucleotide 79 to nucleotide 2424;

(c) the nucleotide sequence of SEQ ID NO:17 from nucleotide 145 to nucleotide 2424;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vk6_1 deposited with the ATCC under accession number 361;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vk6_1 deposited with the ATCC under accession number 361;

(f) the nucleotide sequence of a mature protein coding sequence of clone vk6_1 deposited with the ATCC under accession number 361;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vk6_1 deposited with the ATCC under accession number 361;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:17.

27. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:18;

(b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone vk6_1 deposited with the ATCC under accession number 361;

the protein being substantially free from other mammalian proteins.

28. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:19;
- (b) the nucleotide sequence of SEQ ID NO:19 from nucleotide 2 to nucleotide 733;
- (c) the nucleotide sequence of SEQ ID NO:19 from nucleotide 71 to nucleotide 733;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo4_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo4_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo4_1 deposited with the ATCC under accession number 361;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo4_1 deposited with the ATCC under accession number 361;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:19.

29. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;

- (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo4_1 deposited with the ATCC under accession number 361;
- the protein being substantially free from other mammalian proteins.

30. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:21;
- (b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 151 to nucleotide 1323;
- (c) the nucleotide sequence of SEQ ID NO:21 from nucleotide 217 to nucleotide 1323;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo8_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo8_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo8_1 deposited with the ATCC under accession number 361;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo8_1 deposited with the ATCC under accession number 361;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:21.

31. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo8_1 deposited with the ATCC under accession number 361;
- the protein being substantially free from other mammalian proteins.

32. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:23;
- (b) the nucleotide sequence of SEQ ID NO:23 from nucleotide 134 to nucleotide 613;
- (c) the nucleotide sequence of SEQ ID NO:23 from nucleotide 215 to nucleotide 613;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo10_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo10_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo10_1 deposited with the ATCC under accession number 361;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo10_1 deposited with the ATCC under accession number 361;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:23.

33. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

(b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo10_1 deposited with the ATCC under accession number 361;

the protein being substantially free from other mammalian proteins.

34. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:25;

(b) the nucleotide sequence of SEQ ID NO:25 from nucleotide 102 to nucleotide 1163;

(c) the nucleotide sequence of SEQ ID NO:25 from nucleotide 156 to nucleotide 1163;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo20_1 deposited with the ATCC under accession number 361;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo20_1 deposited with the ATCC under accession number 361;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo20_1 deposited with the ATCC under accession number 361;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo20_1 deposited with the ATCC under accession number 361;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:26;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:25.

35. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:26;

(b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo20_1 deposited with the ATCC under accession number 361;

the protein being substantially free from other mammalian proteins.

36. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:27;
- (b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 67 to nucleotide 702;
- (c) the nucleotide sequence of SEQ ID NO:27 from nucleotide 157 to nucleotide 702;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo21_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo21_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo21_1 deposited with the ATCC under accession number 361;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo21_1 deposited with the ATCC under accession number 361;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:27.

37. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;

- (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo21_1 deposited with the ATCC under accession number 361;
- the protein being substantially free from other mammalian proteins.

38. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:29;
- (b) the nucleotide sequence of SEQ ID NO:29 from nucleotide 57 to nucleotide 272;
- (c) the nucleotide sequence of SEQ ID NO:29 from nucleotide 114 to nucleotide 272;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp24_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp24_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp24_1 deposited with the ATCC under accession number 361;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp24_1 deposited with the ATCC under accession number 361;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:29.

39. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vp24_1 deposited with the ATCC under accession number 361;
- the protein being substantially free from other mammalian proteins.

40. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:31;
- (b) the nucleotide sequence of SEQ ID NO:31 from nucleotide 38 to nucleotide 757;
- (c) the nucleotide sequence of SEQ ID NO:31 from nucleotide 137 to nucleotide 757;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo17_1 deposited with the ATCC under accession number 361;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo17_1 deposited with the ATCC under accession number 361;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo17_1 deposited with the ATCC under accession number 361;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo17_1 deposited with the ATCC under accession number 361;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:31.

41. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:32;

(b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo17_1 deposited with the ATCC under accession number 361;

the protein being substantially free from other mammalian proteins.

42. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:33;

(b) the nucleotide sequence of SEQ ID NO:33 from nucleotide 93 to nucleotide 263;

(c) the nucleotide sequence of SEQ ID NO:33 from nucleotide 174 to nucleotide 263;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq11_1 deposited with the ATCC under accession number PTA-367;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq11_1 deposited with the ATCC under accession number PTA-367;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq11_1 deposited with the ATCC under accession number PTA-367;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq11_1 deposited with the ATCC under accession number PTA-367;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:33.

43. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:34;

(b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq11_1 deposited with the ATCC under accession number PTA-367;

the protein being substantially free from other mammalian proteins.

44. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:35;
- (b) the nucleotide sequence of SEQ ID NO:35 from nucleotide 43 to nucleotide 1125;
- (c) the nucleotide sequence of SEQ ID NO:35 from nucleotide 85 to nucleotide 1125;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq12_1 deposited with the ATCC under accession number PTA-367;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq12_1 deposited with the ATCC under accession number PTA-367;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq12_1 deposited with the ATCC under accession number PTA-367;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq12_1 deposited with the ATCC under accession number PTA-367;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:35.

45. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;

- (b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vq12_1 deposited with the ATCC under accession number PTA-367; the protein being substantially free from other mammalian proteins.

46. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:37;
- (b) the nucleotide sequence of SEQ ID NO:37 from nucleotide 32 to nucleotide 904;
- (c) the nucleotide sequence of SEQ ID NO:37 from nucleotide 77 to nucleotide 904;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq14_1 deposited with the ATCC under accession number PTA-367;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq14_1 deposited with the ATCC under accession number PTA-367;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq14_1 deposited with the ATCC under accession number PTA-367;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq14_1 deposited with the ATCC under accession number PTA-367;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:37.

47. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
- (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vq14_1 deposited with the ATCC under accession number PTA-367;

the protein being substantially free from other mammalian proteins.

48. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:39;
- (b) the nucleotide sequence of SEQ ID NO:39 from nucleotide 384 to nucleotide 1193;
- (c) the nucleotide sequence of SEQ ID NO:39 from nucleotide 642 to nucleotide 1193;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq15_1 deposited with the ATCC under accession number PTA-367;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq15_1 deposited with the ATCC under accession number PTA-367;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq15_1 deposited with the ATCC under accession number PTA-367;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq15_1 deposited with the ATCC under accession number PTA-367;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:40;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:39.

49. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:40;

(b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq15_1 deposited with the ATCC under accession number PTA-367;

the protein being substantially free from other mammalian proteins.

50. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:41;

(b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 132 to nucleotide 503;

(c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 189 to nucleotide 503;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq17_1 deposited with the ATCC under accession number PTA-367;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq17_1 deposited with the ATCC under accession number PTA-367;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq17_1 deposited with the ATCC under accession number PTA-367;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq17_1 deposited with the ATCC under accession number PTA-367;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:41.

51. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq17_1 deposited with the ATCC under accession number PTA-367;

the protein being substantially free from other mammalian proteins.

52. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:43;
- (b) the nucleotide sequence of SEQ ID NO:43 from nucleotide 69 to nucleotide 401;
- (c) the nucleotide sequence of SEQ ID NO:43 from nucleotide 138 to nucleotide 401;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq18_1 deposited with the ATCC under accession number PTA-367;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq18_1 deposited with the ATCC under accession number PTA-367;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq18_1 deposited with the ATCC under accession number PTA-367;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq18_1 deposited with the ATCC under accession number PTA-367;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:44;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:43.

53. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:44;

- (b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vq18_1 deposited with the ATCC under accession number PTA-367; the protein being substantially free from other mammalian proteins.

54. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:45;
- (b) the nucleotide sequence of SEQ ID NO:45 from nucleotide 65 to nucleotide 1180;
- (c) the nucleotide sequence of SEQ ID NO:45 from nucleotide 149 to nucleotide 1180;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq22_1 deposited with the ATCC under accession number PTA-367;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq22_1 deposited with the ATCC under accession number PTA-367;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq22_1 deposited with the ATCC under accession number PTA-367;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq22_1 deposited with the ATCC under accession number PTA-367;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:45.

55. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq22_1 deposited with the ATCC under accession number PTA-367;
- the protein being substantially free from other mammalian proteins.

56. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:47;
- (b) the nucleotide sequence of SEQ ID NO:47 from nucleotide 18 to nucleotide 1409;
- (c) the nucleotide sequence of SEQ ID NO:47 from nucleotide 60 to nucleotide 1409;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vr3_1 deposited with the ATCC under accession number PTA-367;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vr3_1 deposited with the ATCC under accession number PTA-367;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vr3_1 deposited with the ATCC under accession number PTA-367;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vr3_1 deposited with the ATCC under accession number PTA-367;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:47.

57. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:48;

(b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and

(c) the amino acid sequence encoded by the cDNA insert of clone vr3_1 deposited with the ATCC under accession number PTA-367;

the protein being substantially free from other mammalian proteins.

58. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:49;

(b) the nucleotide sequence of SEQ ID NO:49 from nucleotide 690 to nucleotide 2570;

(c) the nucleotide sequence of SEQ ID NO:49 from nucleotide 765 to nucleotide 2570;

(d) the nucleotide sequence of SEQ ID NO:49 from nucleotide 1286 to nucleotide 2895;

(e) the nucleotide sequence of the full-length protein coding sequence of clone vb26_1 deposited with the ATCC under accession number PTA-367;

(f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb26_1 deposited with the ATCC under accession number PTA-367;

(g) the nucleotide sequence of a mature protein coding sequence of clone vb26_1 deposited with the ATCC under accession number PTA-367;

(h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb26_1 deposited with the ATCC under accession number PTA-367;

(i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:50;

(j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and

(l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:49.

59. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:50;

(b) the amino acid sequence of SEQ ID NO:50 from amino acid 200 to amino acid 627;

(c) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and

(d) the amino acid sequence encoded by the cDNA insert of clone vb26_1 deposited with the ATCC under accession number PTA-367;

the protein being substantially free from other mammalian proteins.

60. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:51;
- (b) the nucleotide sequence of SEQ ID NO:51 from nucleotide 105 to nucleotide 1724;
- (c) the nucleotide sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1724;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc70_1 deposited with the ATCC under accession number PTA-367;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc70_1 deposited with the ATCC under accession number PTA-367;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc70_1 deposited with the ATCC under accession number PTA-367;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc70_1 deposited with the ATCC under accession number PTA-367;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:51.

31. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vc70_1 deposited with the ATCC under accession number PTA-367;
- the protein being substantially free from other mammalian proteins.

62. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:53;
- (b) the nucleotide sequence of SEQ ID NO:53 from nucleotide 3 to nucleotide 239;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone vo28_1 deposited with the ATCC under accession number PTA-367;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo28_1 deposited with the ATCC under accession number PTA-367;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:54;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:53.

63. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:54;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo28_1 deposited with the ATCC under accession number PTA-367;
- the protein being substantially free from other mammalian proteins.

64. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:55;
- (b) the nucleotide sequence of SEQ ID NO:55 from nucleotide 49 to nucleotide 1452;
- (c) the nucleotide sequence of SEQ ID NO:55 from nucleotide 109 to nucleotide 1452;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo29_1 deposited with the ATCC under accession number PTA-367;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo29_1 deposited with the ATCC under accession number PTA-367;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo29_1 deposited with the ATCC under accession number PTA-367;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo29_1 deposited with the ATCC under accession number PTA-367;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:55.

65. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo29_1 deposited with the ATCC under accession number PTA-367;

the protein being substantially free from other mammalian proteins.

66. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:57;

(b) the nucleotide sequence of SEQ ID NO:57 from nucleotide 48 to nucleotide 866;

(c) the nucleotide sequence of SEQ ID NO:57 from nucleotide 114 to nucleotide 866;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo30_1 deposited with the ATCC under accession number PTA-367;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo30_1 deposited with the ATCC under accession number PTA-367;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo30_1 deposited with the ATCC under accession number PTA-367;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo30_1 deposited with the ATCC under accession number PTA-367;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:58;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:57.

67. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:58;

(b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo30_1 deposited with the ATCC under accession number PTA-367;

the protein being substantially free from other mammalian proteins.

68. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:59;

(b) the nucleotide sequence of SEQ ID NO:59 from nucleotide 235 to nucleotide 510;

(c) the nucleotide sequence of SEQ ID NO:59 from nucleotide 316 to nucleotide 510;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp25_1 deposited with the ATCC under accession number PTA-367;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp25_1 deposited with the ATCC under accession number PTA-367;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp25_1 deposited with the ATCC under accession number PTA-367;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp25_1 deposited with the ATCC under accession number PTA-367;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:59.

69. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vp25_1 deposited with the ATCC under accession number PTA-367;
- the protein being substantially free from other mammalian proteins.

70. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:61;
- (b) the nucleotide sequence of SEQ ID NO:61 from nucleotide 177 to nucleotide 1626;
- (c) the nucleotide sequence of SEQ ID NO:61 from nucleotide 219 to nucleotide 1626;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq25_1 deposited with the ATCC under accession number PTA-367;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq25_1 deposited with the ATCC under accession number PTA-367;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq25_1 deposited with the ATCC under accession number PTA-367;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq25_1 deposited with the ATCC under accession number PTA-367;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:62;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:61.

71. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:62;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq25_1 deposited with the ATCC under accession number PTA-367;
- the protein being substantially free from other mammalian proteins.

Fig. 1B

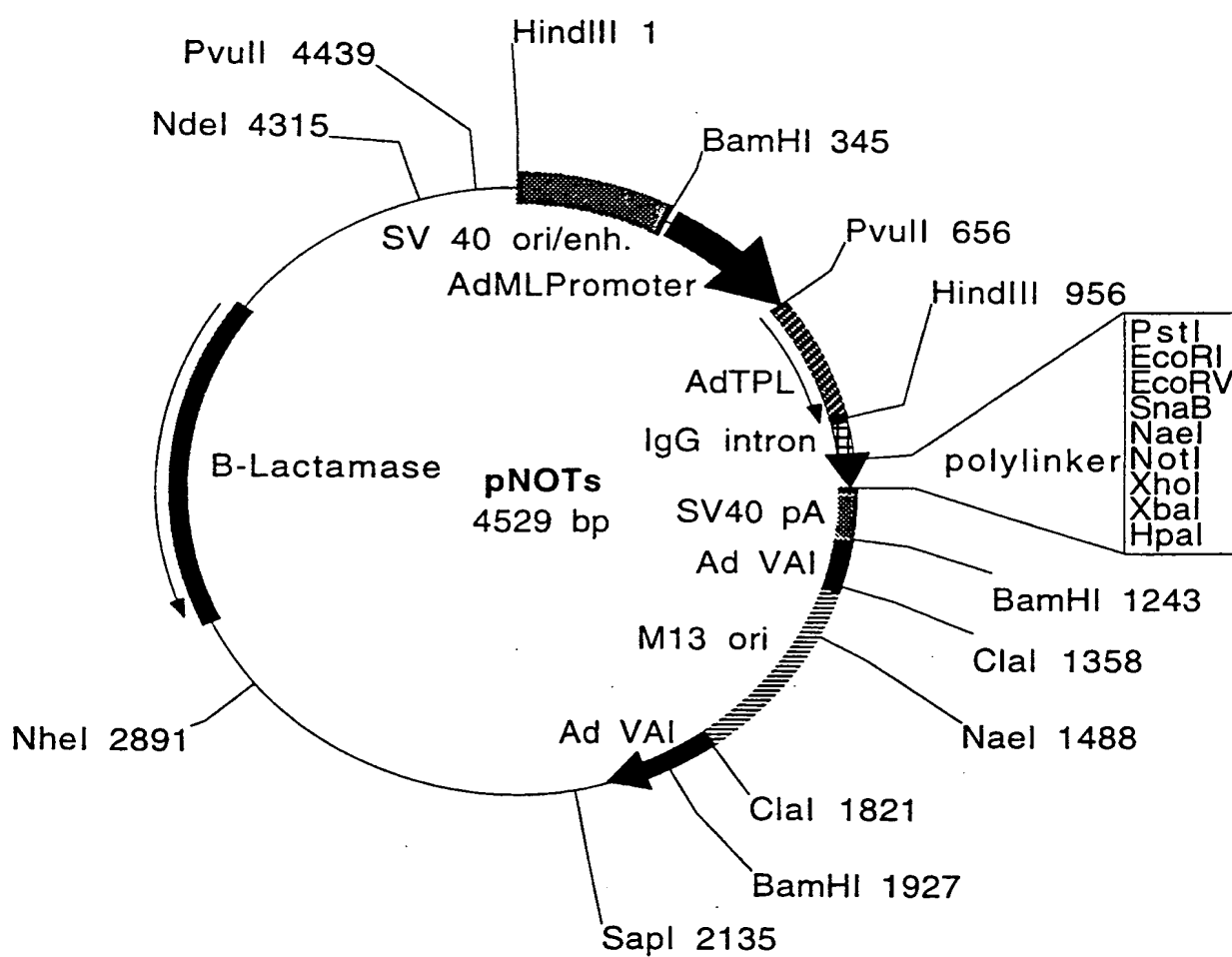
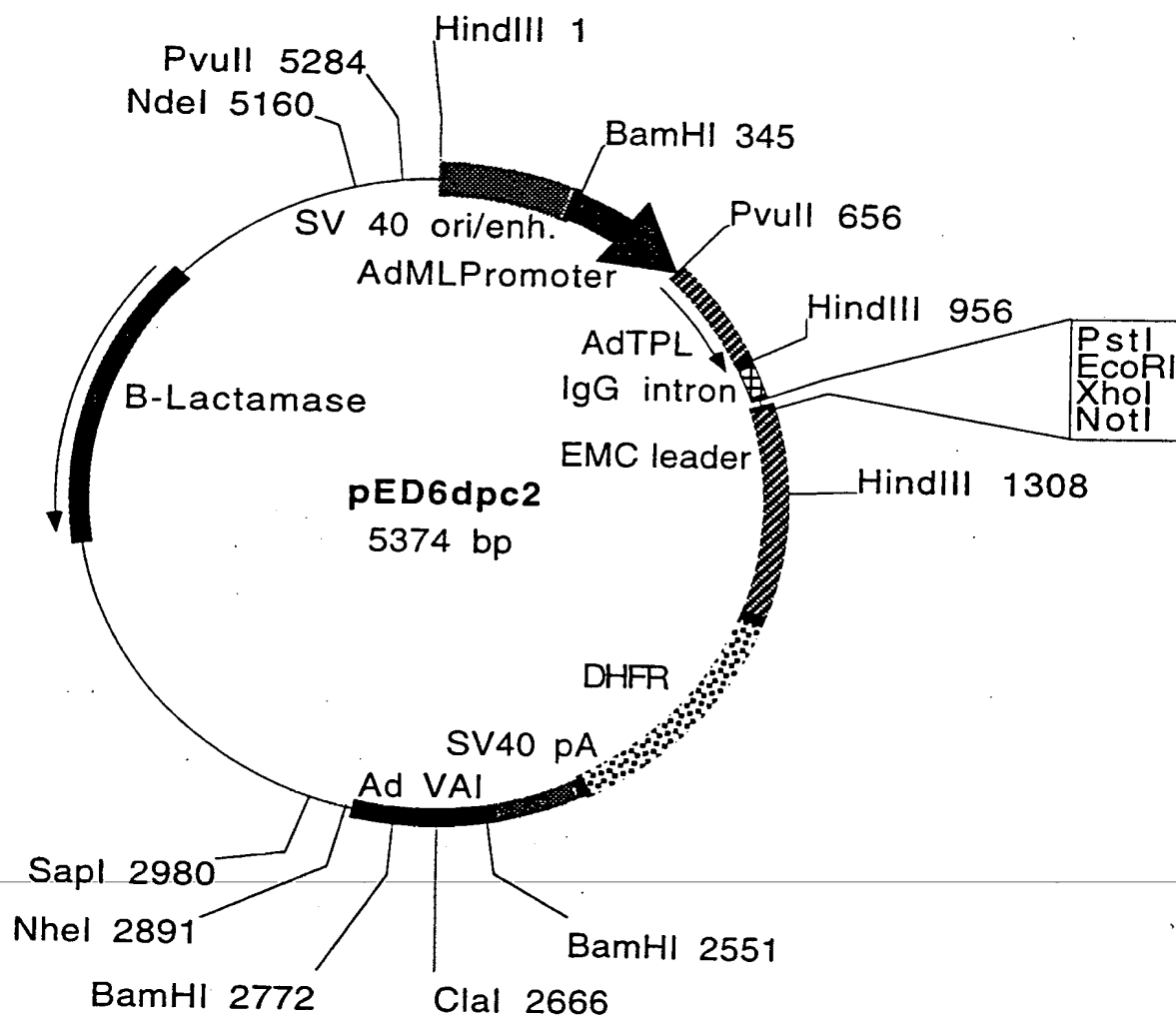


Fig. 1A



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Asn	Ser	Lys	Asn	Ala	Phe	Val	Phe	Leu	Gln	Tyr	Asp	Lys	Asn	Phe	Ile	115	120	125	
Gln	Ile	Arg	Arg	Val	Phe	Pro	Thr	Asn	Phe	Pro	Gly	Leu	Gln	Lys	Lys	130	135	140	
Gly	Glu	Glu	Asp	Gln	Lys	Ser	Phe	Phe	Glu	Phe	Leu	Val	Leu	Asn	Lys	145	150	155	160
Val	Ser	Pro	Ser	Gln	Phe	Gly	Cys	His	Val	Leu	Cys	Thr	Trp	Leu	Glu	165	170	175	
Ser	Cys	Leu	Lys	Ser	Glu	Asn	Gly	Arg	Thr	Glu	Ser	Cys	Gly	Ile	Met	180	185	190	
Tyr	Thr	Lys	Cys	Thr	Cys	Pro	Gln	His	Leu	Gly	Glu	Trp	Gly	Ile	Asp	195	200	205	
Asp	Gln	Ser	Leu	Ile	Leu	Leu	Asn	Asn	Val	Val	Leu	Pro	Leu	Asn	Glu	210	215	220	
Gln	Thr	Glu	Gly	Cys	Leu	Thr	Gln	Glu	Leu	Gln	Thr	Thr	Gln	Val	Cys	225	230	235	240
Asn	Leu	Thr	Arg	Glu	Ala	Lys	Arg	Pro	Pro	Lys	Glu	Glu	Phe	Gly	Met	245	250	255	

Met Gly Asp His Thr Ile Lys Ser Gln Arg Pro Arg Ser Val His Glu
 260 265 270
 Lys Arg Val Pro Gln Glu Gln Ala Asp Ala Ala Lys Phe Met Ala Gln
 275 280 285
 Thr Gly Glu Ser Gly Val Glu Glu Trp Ser Gln Trp Ser Thr Cys Ser
 290 295 300
 Val Thr Cys Gly Gln Gly Ser Gln Val Arg Thr Arg Thr Cys Val Ser
 305 310 315 320
 Pro Tyr Gly Thr His Cys Ser Gly Pro Leu Arg Glu Ser Arg Val Cys
 325 330 335
 Asn Asn Thr Ala Leu Cys Pro Val His Gly Val Trp Glu Glu Trp Ser
 340 345 350
 Pro Trp Ser Leu Cys Ser Phe Thr Cys Gly Arg Gly Gln Arg Thr Arg
 355 360 365
 Thr Arg Ser Cys Thr Pro Pro Gln Tyr Gly Gly Arg Pro Cys Glu Gly
 370 375 380
 Pro Glu Thr His His Lys Pro Cys Asn Ile Ala Leu Cys Pro Val Asp
 385 390 395 400
 Gly Gln Trp Gln Glu Trp Ser Ser Trp Ser Gln Cys Ser Val Thr Cys
 405 410 415
 Ser Asn Gly Thr Gln Gln Arg Ser Arg Gln Cys Thr Ala Ala Ala His
 420 425 430
 Gly Gly Ser Glu Cys Arg Gly Pro Trp Ala Glu Ser Arg Glu Cys Tyr
 435 440 445
 Asn Pro Glu Cys Thr Ala Asn Gly Gln Trp Asn Gln Trp Gly His Trp
 450 455 460
 Ser Gly Cys Ser Lys Ser Cys Asp Gly Gly Trp Glu Arg Arg Ile Arg
 465 470 475 480
 Thr Cys Gln Gly Ala Val Ile Thr Gly Gln Gln Cys Glu Gly Thr Gly
 485 490 495
 Glu Glu Val Arg Arg Cys Ser Glu Gln Arg Cys Pro Ala Pro Tyr Glu
 500 505 510
 Ile Cys Pro Glu Asp Tyr Leu Met Ser Met Val Trp Lys Arg Thr Pro
 515 520 525
 Ala Gly Asp Leu Ala Phe Asn Gln Cys Pro Leu Asn Ala Thr Gly Thr
 530 535 540
 Thr Ser Arg Arg Cys Ser Leu Ser Leu His Gly Val Ala Phe Trp Glu
 545 550 555 560
 Gln Pro Ser Phe Ala Arg Cys Ile Ser Asn Glu Tyr Arg His Leu Gln
 565 570 575

His Ser Ile Lys Glu His Leu Ala Lys Gly Gln Arg Met Leu Ala Gly
 580 585 590
 Asp Gly Met Ser Gln Val Thr Lys Thr Leu Leu Asp Leu Thr Gln Arg
 595 600 605
 Lys Asn Phe Tyr Ala Gly Asp Leu Leu Met Ser Val Glu Ile Leu Arg
 610 615 620
 Asn Val Thr Asp Thr Phe Lys Arg Ala Ser Tyr Ile Pro Ala Ser Asp
 625 630 635 640
 Gly Val Gln Asn Phe Phe Gln Ile Val Ser Asn Leu Leu Asp Glu Glu
 645 650 655
 Asn Lys Glu Lys Trp Glu Asp Ala Gln Gln Ile Tyr Pro Gly Ser Ile
 660 665 670
 Glu Leu Met Gln Val Ile Glu Asp Phe Ile His Ile Val Gly Met Gly
 675 680 685
 Met Met Asp Phe Gln Asn Ser Tyr Leu Met Thr Gly Asn Val Val Ala
 690 695 700
 Ser Ile Gln Lys Leu Pro Ala Ala Ser Val Leu Thr Asp Ile Asn Phe
 705 710 715 720
 Pro Met Lys Gly Arg Lys Gly Met Val Asp Trp Ala Arg Asn Ser Glu
 725 730 735
 Asp Arg Val Val Ile Pro Lys Ser Ile Phe Thr Pro Val Ser Ser Lys
 740 745 750
 Glu Leu Asp Glu Ser Ser Val Phe Val Leu Gly Ala Val Leu Tyr Lys
 755 760 765
 Asn Leu Asp Leu Ile Leu Pro Thr Leu Arg Asn Tyr Thr Val Ile Asn
 770 775 780
 Ser Lys Ile Ile Val Val Thr Ile Arg Pro Glu Pro Lys Thr Thr Asp
 785 790 795 800
 Ser Phe Leu Glu Ile Glu Leu Ala His Leu Ala Asn Gly Thr Leu Asn
 805 810 815
 Pro Tyr Cys Val Leu Trp Asp Asp Ser Lys Thr Asn Glu Ser Leu Gly
 820 825 830
 Thr Trp Ser Thr Gln Gly Cys Lys Thr Val Leu Thr Asp Ala Ser His
 835 840 845
 Thr Lys Cys Leu Cys Asp Arg Leu Ser Thr Phe Ala Ile Leu Ala Gln
 850 855 860
 Gln Pro Arg Glu Ile Ile Met Glu Ser Ser Gly Thr Pro Ser Val Thr
 865 870 875 880
 Leu Ile Val Gly Ser Gly Leu Ser Cys Leu Ala Leu Ile Thr Leu Ala
 885 890 895

Val Val Tyr Ala Ala Leu Trp Arg Tyr Ile Arg Ser Glu Arg Ser Ile
 900 905 910
 Ile Leu Ile Asn Phe Cys Leu Ser Ile Ile Ser Ser Asn Ile Leu Ile
 915 920 925
 Leu Val Gly Gln Thr Gln Thr His Asn Lys Ser Ile Cys Thr Thr Thr
 930 935 940
 Thr Ala Phe Leu His Phe Phe Phe Leu Ala Ser Phe Cys Trp Val Leu
 945 950 955 960
 Thr Glu Ala Trp Gln Ser Tyr Met Ala Val Thr Gly Lys Ile Arg Thr
 965 970 975
 Arg Leu Ile Arg Lys Arg Phe Leu Cys Leu Gly Trp Gly Leu Pro Ala
 980 985 990
 Leu Val Val Ala Thr Ser Val Gly Phe Thr Arg Thr Lys Gly Tyr Gly
 995 1000 1005
 Thr Asp His Tyr Cys Trp Leu Ser Leu Glu Gly Gly Leu Leu Tyr Ala
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 Phe Val Gly Pro Ala Ala Ala Val Val Leu Val Asn Met Val Ile Gly
 1025 1030 1035 1040
 Ile Leu Val Phe Asn Lys Leu Val Ser Arg Asp Gly Ile Leu Asp Lys
 1045 1050 1055
 Lys Leu Lys His Arg Ala Gly Gln Met Ser Glu Pro His Ser Gly Leu
 1060 1065 1070
 Thr Leu Lys Cys Ala Lys Cys Gly Val Val Ser Thr Thr Ala Leu Ser
 1075 1080 1085
 Ala Thr Thr Ala Ser Asn Ala Met Ala Ser Leu Trp Ser Ser Cys Val
 1090 1095 1100
 Val Leu Pro Leu Leu Ala Leu Thr Trp Met Ser Ala Val Leu Ala Met
 1105 1110 1115 1120
 Thr Asp Lys Arg Ser Ile Leu Phe Gln Ile Leu Phe Ala Val Phe Asp
 1125 1130 1135
 Ser Leu Gln Gly Phe Val Ile Val Met Val His Cys Ile Leu Arg Arg
 1140 1145 1150
 Glu Val Gln Asp Ala Phe Arg Cys Arg Leu Arg Asn Cys Gln Asp Pro
 1155 1160 1165
 Ile Asn Ala Asp Ser Ser Ser Ser Phe Pro Asn Gly His Ala Gln Ile
 1170 1175 1180
 Met Thr Asp Phe Glu Lys Asp Val Asp Ile Ala Cys Arg Ser Val Leu
 1185 1190 1195 1200
 His Lys Asp Ile Gly Pro Cys Arg Ala Ala Thr Ile Thr Gly Thr Leu
 1205 1210 1215

Ser Arg Ile Ser Leu Asn Asp Asp Glu Glu Glu Lys Gly Thr Asn Pro
 1220 1225 1230
 Glu Gly Leu Ser Tyr Ser Thr Leu Pro Gly Asn Val Ile Ser Lys Val
 1235 1240 1245
 Ile Ile Gln Gln Pro Thr Gly Leu His Met Pro Met Ser Met Asn Glu
 1250 1255 1260
 Leu Ser Asn Pro Cys Leu Lys Lys Glu Asn Ser Glu Leu Arg Arg Thr
 1265 1270 1275 1280
 Val Tyr Leu Cys Thr Asp Asp Asn Leu Arg Gly Ala Asp Met Asp Ile
 1285 1290 1295
 Val His Pro Gln Glu Arg Met Met Glu Ser Asp Tyr Ile Val Met Pro
 1300 1305 1310
 Arg Ser Ser Val Asn Asn Gln Pro Ser Met Lys Glu Glu Ser Lys Met
 1315 1320 1325
 Asn Ile Gly Met Glu Thr Leu Pro His Glu Arg Leu Leu His Tyr Lys
 1330 1335 1340
 Val Asn Pro Glu Phe Asn Met Asn Pro Pro Val Met Asp Gln Phe Asn
 1345 1350 1355 1360
 Met Asn Leu Glu Gln His Leu Ala Pro Gln Glu His Met Gln Asn Leu
 1365 1370 1375
 Pro Phe Glu Pro Arg Thr Ala Val Lys Asn Phe Met Ala Ser Glu Leu
 1380 1385 1390
 Asp Asp Asn Ala Gly Leu Ser Arg Ser Glu Thr Gly Ser Thr Ile Ser
 1395 1400 1405
 Met Ser Ser Leu Glu Arg Arg Lys Ser Arg Tyr Ser Asp Leu Asp Phe
 1410 1415 1420
 Glu Lys Val Met His Thr Arg Lys Arg His Met Glu Leu Phe Gln Glu
 1425 1430 1435 1440
 Leu Asn Gln Lys Phe Gln Thr Leu Asp Arg Phe Arg Asp Ile Pro Asn
 1445 1450 1455
 Thr Ser Ser Met Glu Asn Pro Ala Pro Asn Lys Asn Pro Trp Asp Thr
 1460 1465 1470
 Phe Lys Asn Pro Ser Glu Tyr Pro His Tyr Thr Thr Ile Asn Val Leu
 1475 1480 1485
 Asp Thr Glu Ala Lys Asp Ala Leu Glu Leu Arg Pro Ala Glu Trp Glu
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 Lys Cys Leu Asn Leu Pro Leu Asp Val Gln Glu Gly Asp Phe Gln Thr
 1505 1510 1515 1520
 Glu Val

<210> 3
 <211> 1955
 <212> DNA
 <213> Homo sapiens

<400> 3

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tgctgggcat cgccttgctg gcctacgtcg cctctgtttg gggcaacttc gttaatatga 180
ggtctatcca ggaaaatggt gaactaaaaa ttgaaagcaa gattgaagag atggttgaac 240
cactaagaga gaaaatcaga gatthagaaa aaagctttac ccagaaatac ccaccagtaa 300
agtttttatt agaaaaggat cggaaaagaa ttttgataac aggaggcgca gggttcgtgg 360
gctcccattc aactgacaaa ctcatgatgg acggccacga ggtgaccgtg gtggacaatt 420
tcttcacgtg caggaagaga aacgtggagc actggatcgg acatgagAAC ttcgagttga 480
ttaaccacga cgtggtggag cccctctaca tcgaggttga ccagatatac catctggcat 540
ctccagcctc cctccaaac tacatgtata atcctatcaa gacattaaag accaatacga 600
ttgggacatt aaacatgttg gggctggcaa aacgagtcgg tgcctcgtctg ctccctggcct 660
ccacatcgga ggtgtatgga gatcctgaag tccaccctca aagtgaggat tactggggcc 720
acgtgaatcc aataggacct cgggcctgct acgatgaagg caaacgtgtt gcagagacca 780
tgtgctatgc ctacatgaag caggaaggcg tggaagtgcg agtgggcaga atcttcaaca 840
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caaggatatt tgaatcact actgtgtttt gctgcgtatc tggggcgggg gcaggttggg 1860
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ttgaaactca ccaaaaaaaa aaaaaaaaaa aaaaaa 1955

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<210> 4
 <211> 357
 <212> PRT
 <213> Homo sapiens

<400> 4

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Met Val Ser Lys Ala Leu Leu Arg Leu Val Ser Ala Val Asn Arg Arg
 1             5             10             15

Arg Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser
      20             25             30

Val Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu
      35             40             45

Leu Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu
      50             55             60

Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val

```

65		70		75		80
Lys Phe Leu Ser Glu	Lys Asp Arg Lys Arg	Ile Leu Ile Thr Gly	Gly			
85	90	95				
Ala Gly Phe Val Gly	Ser His Leu Thr Asp	Lys Leu Met Met Asp	Gly			
100	105	110				
His Glu Val Thr Val	Val Asp Asn Phe Phe Thr	Gly Arg Lys Arg Asn				
115	120	125				
Val Glu His Trp Ile	Gly His Glu Asn Phe Glu	Leu Ile Asn His Asp				
130	135	140				
Val Val Glu Pro Leu	Tyr Ile Glu Val Asp	Gln Ile Tyr His Leu	Ala			
145	150	155	160			
Ser Pro Ala Ser Pro	Pro Asn Tyr Met Tyr	Asn Pro Ile Lys Thr	Leu			
165	170	175				
Lys Thr Asn Thr Ile	Gly Thr Leu Asn Met	Leu Gly Leu Ala Lys	Arg			
180	185	190				
Val Gly Ala Arg Leu	Leu Leu Ala Ser Thr	Ser Glu Val Tyr Gly	Asp			
195	200	205				
Pro Glu Val His Pro	Gln Ser Glu Asp Tyr	Trp Gly His Val Asn	Pro			
210	215	220				
Ile Gly Pro Arg Ala	Cys Tyr Asp Glu Gly	Lys Arg Val Ala Glu	Thr			
225	230	235	240			
Met Cys Tyr Ala Tyr	Met Lys Gln Glu Gly	Val Glu Val Arg Val	Ala			
245	250	255				
Arg Ile Phe Asn Thr	Phe Gly Pro Arg Met	His Met Asn Asp Gly	Arg			
260	265	270				
Val Val Ser Asn Phe	Ile Leu Gln Ala Leu	Gln Gly Glu Pro Leu	Thr			
275	280	285				
Val Tyr Gly Ser Gly	Ser Gln Thr Arg Ala	Phe Gln Tyr Val Ser	Asp			
290	295	300				
Leu Val Asn Gly Leu	Val Ala Leu Met Asn	Ser Asn Val Ser Ser	Pro			
305	310	315	320			
Val Asn Leu Gly Asn	Pro Glu Glu His Thr	Ile Leu Glu Phe Ala	Gln			
325	330	335				
Leu Ile Lys Asn Leu	Val Gly Pro Ala Gly	Gly Arg Phe Lys Gln	Ser			
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Asn Ser Leu Leu Pro						
355						

<210> 5

<211> 1874

<212> DNA

<213> Homo sapiens

<400> 5

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ggattcattc attttctgaa ttctctatgt gaggacagta ttagagccca gtgagggttt 180
gagaggcccc aaagatgagc gccaacagca gcagagtggg ccagcttctc ttgcagggtt 240
cagcgtgcat taggtggaag caggatgtgg aaggggctat ctaccaccta gccaaactgcc 300
tcttactcct gggcttcatg gggggcagtg ggggtgatgg atgcttctat ctttttggct 360
tcctgagtgc aggttacctg tgctgcgtgc tgtggggctg gttcagtgcc tgtggcctgg 420
acattgttct ttggagcttc ctgctggctg ttgtctgcct gctccagctg gcacacctgg 480
tataccgcct gcgtgaggac accctccctg aggagtttga cctcctctac aagacgctgt 540
gcctgccctt gcaggtgccc ctacagacat acaaggagat tgttactgct tgtgaggagc 600
aggtcttaac tctggccact gaacagacct atgctgtgga gggtagagaca cccatcaacc 660
gcctgtccct gctgctctct ggccgggttc gtgtgagcca ggatgggcag tttctgcact 720
acatctttcc ataccagttc atggactctc ctgagtggga atcactacag cttctgagg 780
aggggggtgt ccaggctact ctgactgctg agacctcatg tagctacatt tctggcccc 840
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tgggtgagga ctccaccagt ctggtgctgg aggttttga ggaggtgtca ggatcagaat 1260
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cacgcctctt tttccaccca ctggaaggct cacaggcaag gtgagagagg acacagaagg 1560
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gaaacccacc tcacagggtt gttgtgagga tccaatgagt tgatttaggt aagcacctag 1800
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aaaaaaaaaa aaaa 1874

```

<210> 6

<211> 368

<212> PRT

<213> Homo sapiens

<400> 6

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Met Ser Ala Asn Ser Ser Arg Val Gly Gln Leu Leu Leu Gln Gly Ser
  1              5              10              15

```

```

Ala Cys Ile Arg Trp Lys Gln Asp Val Glu Gly Ala Ile Tyr His Leu
      20              25              30

```

```

Ala Asn Cys Leu Leu Leu Leu Gly Phe Met Gly Gly Ser Gly Val Tyr
      35              40              45

```

```

Gly Cys Phe Tyr Leu Phe Gly Phe Leu Ser Ala Gly Tyr Leu Cys Cys
      50              55              60

```

```

Val Leu Trp Gly Trp Phe Ser Ala Cys Gly Leu Asp Ile Val Leu Trp
      65              70              75              80

```

```

Ser Phe Leu Leu Ala Val Val Cys Leu Leu Gln Leu Ala His Leu Val
      85              90              95

```

Tyr Arg Leu Arg Glu Asp Thr Leu Pro Glu Glu Phe Asp Leu Leu Tyr
 100 105 110
 Lys Thr Leu Cys Leu Pro Leu Gln Val Pro Leu Gln Thr Tyr Lys Glu
 115 120 125
 Ile Val His Cys Cys Glu Glu Gln Val Leu Thr Leu Ala Thr Glu Gln
 130 135 140
 Thr Tyr Ala Val Glu Gly Glu Thr Pro Ile Asn Arg Leu Ser Leu Leu
 145 150 155 160
 Leu Ser Gly Arg Val Arg Val Ser Gln Asp Gly Gln Phe Leu His Tyr
 165 170 175
 Ile Phe Pro Tyr Gln Phe Met Asp Ser Pro Glu Trp Glu Ser Leu Gln
 180 185 190
 Pro Ser Glu Glu Gly Val Phe Gln Val Thr Leu Thr Ala Glu Thr Ser
 195 200 205
 Cys Ser Tyr Ile Ser Trp Pro Arg Lys Ser Leu His Leu Leu Leu Thr
 210 215 220
 Lys Glu Arg Tyr Ile Ser Cys Leu Phe Ser Ala Leu Leu Gly Tyr Asp
 225 230 235 240
 Ile Ser Glu Lys Leu Tyr Thr Leu Asn Asp Lys Leu Phe Ala Lys Phe
 245 250 255
 Gly Leu Arg Phe Asp Ile Arg Leu Pro Ser Leu Tyr His Val Leu Gly
 260 265 270
 Pro Thr Ala Ala Asp Ala Gly Pro Glu Ser Glu Lys Gly Asp Glu Glu
 275 280 285
 Val Cys Glu Pro Ala Val Ser Pro Pro Gln Ala Thr Pro Thr Ser Leu
 290 295 300
 Gln Gln Thr Pro Pro Cys Ser Thr Pro Pro Ala Thr Thr Asn Phe Pro
 305 310 315 320
 Ala Pro Pro Thr Arg Ala Arg Leu Ser Arg Pro Asp Ser Gly Ile Leu
 325 330 335
 Gly Glu Asp Ser Thr Ser Leu Val Leu Glu Asp Phe Glu Glu Val Ser
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 Gly Ser Glu Ser Phe Met Asp Tyr Arg Ser Asp Gly Glu Tyr Met Arg
 355 360 365

<210> 7

<211> 782

<212> DNA

<213> Homo sapiens

<400> 7

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gccagtcacat gaccctgcgc ccctcactcc tcccgcctcca tctgctgctg ctgctgctgc 180
tcagtgcggc ggtgtgccgg gctgaggctg ggctcgaaac cgaaagtcct gtcgggaccc 240
tccaagtggg gaccctggtg gagccccag aaccatgtgc cgagcccgt gcttttggag 300
acacgcttca catacactac acgggaagct tggtagatgg acgtattatt gacacctccc 360
tgaccagaga ccctctggtt atagaacttg gccaaaagca ggtgattcca ggtctggagc 420
agagtcttct cgacatgtgt gtgggagaga agcgaagggc aatcattcct tctcacttgg 480
cctatggaaa acgggggattt ccaccatctg tcccagcgga tgcagtgggt cagtatgacg 540
tggagctgat tgcactaatc cgagccaact actggctaaa gctgggtgaag ggcattttgc 600
ctctggtagg gatggccatg gtgccagccc tctgggcct cattgggtat cacctataca 660
gaaaggccaa tagaccctaaa gtctccaaaa agaagctcaa ggaagagaaa cgaaacaaga 720
gcaaaaagaa ataataaata ataaatttta aaaaacttaa aaaaaaaaaa aaaaaaaaaa 780
aa

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<210> 8

<211> 201

<212> PRT

<213> Homo sapiens

<400> 8

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Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu Leu Leu
  1                      5                      10                      15

```

```

Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu Thr Glu
      20                      25                      30

```

```

Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu Pro Pro Glu
      35                      40                      45

```

```

Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu His Ile His Tyr
      50                      55                      60

```

```

Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg
      65                      70                      75                      80

```

```

Asp Pro Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly Leu
      85                      90                      95

```

```

Glu Gln Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala Ile
      100                      105                      110

```

```

Ile Pro Ser His Leu Ala Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val
      115                      120                      125

```

```

Pro Ala Asp Ala Val Val Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile
      130                      135                      140

```

```

Arg Ala Asn Tyr Trp Leu Lys Leu Val Lys Gly Ile Leu Pro Leu Val
      145                      150                      155                      160

```

```

Gly Met Ala Met Val Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu
      165                      170                      175

```

```

Tyr Arg Lys Ala Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu
      180                      185                      190

```

```

Glu Lys Arg Asn Lys Ser Lys Lys Lys
      195                      200

```

<210> 9

<211> 1700

<212> DNA

<213> Homo sapiens

<400> 9

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ggccccggcag cttcgccgtt ctatggaaaa cattgagctc gggctgagtg agggccaggt 180
gatgctgggt ctagccagcc acctgagcac agtggagtcg gagaaacaga agctgcgggc 240
tcaggtgcgg cggctatgcc aggagaacca gtggctgcgg gatgagctgg ctggcaccca 300
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agggcatgcc accaaggatt ccctggatga cctctttcct aatgaggagg aagaggaccc 480
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<210> 10

<211> 143

<212> PRT

<213> Homo sapiens

<400> 10

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Ala Gln Val Arg Arg Leu Cys Gln Glu Asn Gln Trp Leu Arg Asp Glu
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Leu Ala Gly Thr Gln Gln Arg Leu Gln Arg Ser Glu Gln Ala Val Ala
                50                      55                      60
Gln Leu Glu Glu Glu Lys Lys His Leu Glu Phe Leu Gly Gln Leu Arg
                65                      70                      75                      80
Gln Tyr Asp Glu Asp Gly His Thr Ser Glu Glu Lys Glu Gly Asp Ala
                85                      90                      95
Thr Lys Asp Ser Leu Asp Asp Leu Phe Pro Asn Glu Glu Glu Asp

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100

105

110

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<211> 781

<212> DNA

<213> Homo sapiens

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<211> 153

<212> PRT

<213> Homo sapiens

<400> 12

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 20 25 30

Trp Pro Arg Val Pro Gln Pro Gln His Ser Ala Gln Ser Leu Ala Trp
 35 40 45

Ser His Leu Met Thr Arg Ser Cys Thr Ser Ser Cys Gly Pro Gly Trp
 50 55 60

Ala Pro Thr Trp Asp Ala His Ser Val Pro Asn Ala Gly Pro Thr Leu
 65 70 75 80

Ser Leu Pro Trp Ala Ala Ser Asp Tyr Asp Trp Leu Arg Gly Gly His
 85 90 95

His Gln Ala Pro Ala Leu His Pro Glu Leu Pro Ser Pro Leu Arg Val
 100 105 110

Leu Gly Pro Gln Lys Pro Cys Cys Ser Leu Thr Cys Asp Gln Val Gln
 115 120 125

Cys Gly Glu Lys Tyr Glu Gly Gly Ser Ser Pro Gly Phe Ser Ser Val
 130 135 140

Arg Asp Pro Cys Pro Ala Pro Ala Pro
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 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Thr Trp Trp Pro Ala Trp Arg Thr Arg Ala Cys Leu Ser Thr Gly Pro
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80

Thr Ser Val Met Trp Phe

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<212> DNA

<213> Homo sapiens

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<211> 331

<212> PRT

<213> Homo sapiens

<400> 16

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 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
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 Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn
 65 70 75 80
 Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val
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 Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His
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 Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp
 115 120 125
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 130 135 140
 Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala
 145 150 155 160
 Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys
 165 170 175
 Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu
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 Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu
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 Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu
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 Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg
 225 230 235 240
 Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu
 245 250 255
 Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser
 260 265 270
 Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys
 275 280 285
 Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe
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Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr
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Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
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<211> 4859
<212> DNA
<213> Homo sapiens

<400> 17

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<210> 18

<211> 782

<212> PRT

<213> Homo sapiens

<400> 18

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Leu Arg Leu Ser Tyr Arg Asp Leu Leu Ser Ala Asn Arg Ser Ala Ile
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Phe Leu Gly Pro Gln Gly Ser Leu Asn Leu Gln Ala Met Tyr Leu Asp
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Glu Tyr Arg Asp Arg Leu Phe Leu Gly Gly Leu Asp Ala Leu Tyr Ser
          65             70             75             80

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Leu Arg Leu Asp Gln Ala Trp Pro Asp Pro Arg Glu Val Leu Trp Pro
          85             90             95

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Pro Gln Pro Gly Gln Arg Glu Glu Cys Val Arg Lys Gly Arg Asp Pro

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		130					135					140			
Leu	Ile	Thr	Val	Gly	His	Arg	Gly	Glu	His	Val	Leu	His	Leu	Glu	Pro
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Gly	Ser	Val	Glu	Ser	Gly	Arg	Gly	Arg	Cys	Pro	His	Glu	Pro	Ser	Arg
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Pro	Phe	Ala	Ser	Thr	Phe	Ile	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Leu	Thr
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Ala	Asp	Phe	Leu	Gly	Arg	Glu	Ala	Met	Ile	Phe	Arg	Ser	Gly	Gly	Pro
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Arg	Pro	Ala	Leu	Arg	Ser	Asp	Ser	Asp	Gln	Ser	Leu	Leu	His	Asp	Pro
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Arg	Phe	Val	Met	Ala	Ala	Arg	Ile	Pro	Glu	Asn	Ser	Asp	Gln	Asp	Asn
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Asp	Lys	Val	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Val	Pro	Ser	Pro	Asp	Gly
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Gly	Ser	Asn	His	Val	Thr	Val	Ser	Arg	Val	Gly	Arg	Val	Cys	Val	Asn
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Asp	Ala	Gly	Gly	Gln	Arg	Val	Leu	Val	Asn	Lys	Trp	Ser	Thr	Phe	Leu
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Lys	Ala	Arg	Leu	Val	Cys	Ser	Val	Pro	Gly	Pro	Gly	Gly	Ala	Glu	Thr
									295					300	
His	Phe	Asp	Gln	Leu	Glu	Asp	Val	Phe	Leu	Leu	Trp	Pro	Lys	Ala	Gly
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				325					330					335	
Gln	Gly	Phe	Ala	Val	Cys	Val	Tyr	His	Met	Ala	Asp	Ile	Trp	Glu	Val
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Pro	Asp	Glu	Val	Leu	Gln	Phe	Ala	Arg	Ala	His	Pro	Leu	Met	Phe	Trp
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Pro	Val	Arg	Pro	Arg	His	Gly	Arg	Pro	Val	Leu	Val	Lys	Thr	His	Leu

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Gly Thr Tyr Asp Val Ile Phe Leu Gly Thr Asp Ser Gly Ser Val Leu		
450	455	460
Lys Val Ile Ala Leu Gln Ala Gly Gly Ser Ala Glu Pro Glu Glu Val		
465	470	475
		480
Val Leu Glu Glu Leu Gln Val Phe Lys Val Pro Thr Pro Ile Thr Glu		
485	490	495
Met Glu Ile Ser Val Lys Arg Gln Met Leu Tyr Val Gly Ser Arg Leu		
500	505	510
Gly Val Ala Gln Leu Arg Leu His Gln Cys Glu Thr Tyr Gly Thr Ala		
515	520	525
Cys Ala Glu Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly		
530	535	540
Ala Ser Cys Thr His Tyr Arg Pro Ser Leu Gly Lys Arg Arg Phe Arg		
545	550	555
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Ser Gln Glu Glu Glu Ala Val Gly Leu Val Ala Ala Thr Met Val Tyr		
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Gly Thr Glu His Asn Ser Thr Phe Leu Glu Cys Leu Pro Lys Ser Pro		
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Gln Ala Ala Val Arg Trp Leu Leu Gln Arg Pro Gly Asp Glu Gly Pro		
610	615	620
Asp Gln Val Lys Thr Asp Glu Arg Val Leu His Thr Glu Arg Gly Leu		
625	630	635
		640
Leu Phe Arg Arg Leu Ser Arg Phe Asp Ala Gly Thr Tyr Thr Cys Thr		
645	650	655
Thr Leu Glu His Gly Phe Ser Gln Thr Val Val Arg Leu Ala Leu Val		
660	665	670
Val Ile Val Ala Ser Gln Leu Asp Asn Leu Phe Pro Pro Glu Pro Lys		
675	680	685
Pro Glu Glu Pro Pro Ala Arg Gly Gly Leu Ala Ser Thr Pro Pro Lys		
690	695	700
Ala Trp Tyr Lys Asp Ile Leu Gln Leu Ile Gly Phe Ala Asn Leu Pro		
705	710	715
		720
Arg Val Asp Glu Tyr Cys Glu Arg Val Trp Cys Arg Gly Thr Thr Glu		
725	730	735
Cys Ser Gly Cys Phe Arg Ser Arg Ser Arg Gly Lys Gln Ala Arg Gly		

740

745

750

Lys Ser Trp Ala Gly Leu Glu Leu Gly Lys Lys Met Lys Ser Arg Val
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His Ala Glu His Asn Arg Thr Pro Arg Glu Val Glu Ala Thr
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<210> 19

<211> 2342

<212> DNA

<213> Homo sapiens

<400> 19

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<210> 20

<211> 244

<212> PRT

<213> Homo sapiens

<400> 20

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Thr Ser Ala Val Ser Phe Ala Thr Gly Ala Leu Gly Met Trp Ile Pro
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Leu Tyr Leu His Arg Ala Gln Val Val Gln Lys Thr Ala Glu Thr Cys
 35 40 45

Asn Ser Pro Pro Cys Gly Ala Lys Asp Ser Leu Ile Phe Gly Ala Ile
 50 55 60

Thr Cys Phe Thr Gly Phe Leu Gly Val Val Thr Gly Ala Gly Ala Thr
 65 70 75 80

Arg Trp Cys Arg Leu Lys Thr Gln Arg Ala Asp Pro Leu Val Cys Ala
 85 90 95

Val Gly Met Leu Gly Ser Ala Ile Phe Ile Cys Leu Ile Phe Val Ala
 100 105 110

Ala Lys Ser Ser Ile Val Gly Ala Tyr Ile Cys Ile Phe Val Gly Glu
 115 120 125

Thr Leu Leu Phe Ser Asn Trp Ala Ile Thr Ala Asp Ile Leu Met Tyr
 130 135 140

Val Val Ile Pro Thr Arg Arg Ala Thr Ala Val Ala Leu Gln Ser Phe
 145 150 155 160

Thr Ser His Leu Leu Gly Asp Ala Gly Ser Pro Tyr Leu Ile Gly Phe
 165 170 175

Ile Ser Asp Leu Ile Arg Gln Ser Thr Lys Asp Ser Pro Leu Trp Glu
 180 185 190

Phe Leu Ser Leu Gly Tyr Ala Leu Met Leu Cys Pro Phe Val Val Val
 195 200 205

Leu Gly Gly Met Phe Phe Leu Ala Thr Val Leu Phe Phe Val Ser Asp
 210 215 220

Arg Ala Arg Ala Glu Gln Gln Val Asn Gln Leu Ala Met Pro Pro Ala
 225 230 235 240

Ser Val Lys Val

<210> 21

<211> 3202

<212> DNA

<213> Homo sapiens

<400> 21

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<210> 22

<211> 391

<212> PRT

<213> Homo sapiens

<400> 22

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His Asp Val Thr Met Ala Gly Leu Gln Glu Leu Arg Phe Pro Glu Glu
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 Lys Pro Leu Leu Arg Gly Gln Asp Ala Thr Glu Leu Glu Ser Ser Asp
 35 40 45
 Ala Phe Leu Leu Ala Ala Asp Thr Asp Trp Lys Glu His Asp Ile Glu
 50 55 60
 Thr Pro Tyr Gly Leu Leu His Val Val Ile Arg Gly Ser Pro Lys Gly
 65 70 75 80
 Asn Arg Pro Ala Ile Leu Thr Tyr His Asp Val Gly Leu Asn His Lys
 85 90 95
 Leu Cys Phe Asn Thr Phe Phe Asn Phe Glu Asp Met Gln Glu Ile Thr
 100 105 110
 Lys His Phe Val Val Cys His Val Asp Ala Pro Gly Gln Gln Val Gly
 115 120 125
 Ala Ser Gln Phe Pro Gln Gly Tyr Gln Phe Pro Ser Met Glu Gln Leu
 130 135 140
 Ala Ala Met Leu Pro Ser Val Val Gln His Phe Gly Phe Lys Tyr Val
 145 150 155 160
 Ile Gly Ile Gly Val Gly Ala Gly Ala Tyr Val Leu Ala Lys Phe Ala
 165 170 175
 Leu Ile Phe Pro Asp Leu Val Glu Gly Leu Val Leu Val Asn Ile Asp
 180 185 190
 Pro Asn Gly Lys Gly Trp Ile Asp Trp Ala Ala Thr Lys Leu Ser Gly
 195 200 205
 Leu Thr Ser Thr Leu Pro Asp Thr Val Leu Ser His Leu Phe Ser Gln
 210 215 220
 Glu Glu Leu Val Asn Asn Thr Glu Leu Val Gln Ser Tyr Arg Gln Gln
 225 230 235 240
 Ile Gly Asn Val Val Asn Gln Ala Asn Leu Gln Leu Phe Trp Asn Met
 245 250 255
 Tyr Asn Ser Arg Arg Asp Leu Asp Ile Asn Arg Pro Gly Thr Val Pro
 260 265 270
 Asn Ala Lys Thr Leu Arg Cys Pro Val Met Leu Val Val Gly Asp Asn
 275 280 285
 Ala Pro Ala Glu Asp Gly Val Val Glu Cys Asn Ser Lys Leu Asp Pro
 290 295 300
 Thr Thr Thr Thr Phe Leu Lys Met Ala Asp Ser Gly Gly Leu Pro Gln
 305 310 315 320
 Val Thr Gln Pro Gly Lys Leu Thr Glu Ala Phe Lys Tyr Phe Leu Gln
 325 330 335

Gly Met Gly Tyr Met Pro Ser Ala Ser Met Thr Arg Leu Ala Arg Ser
 340 345 350

Arg Thr Ala Ser Leu Thr Ser Ala Ser Ser Val Asp Gly Ser Arg Pro
 355 360 365

Gln Ala Cys Thr His Ser Glu Ser Ser Glu Gly Leu Gly Gln Val Asn
 370 375 380

His Thr Met Glu Val Ser Cys
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<210> 23

<211> 1007

<212> DNA

<213> Homo sapiens

<400> 23

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<210> 24

<211> 160

<212> PRT

<213> Homo sapiens

<400> 24

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Trp Leu Ser Gly Leu Ser Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile
 20 25 30

Met Glu Glu Lys Ala Leu Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg
 35 40 45

Asp Pro Glu Lys Pro Asn Thr Leu Glu Glu Leu Glu Val Val Ser Glu
 50 55 60

Ser Cys Val Glu Val Gln Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile
 65 70 75 80

Ile Arg Phe Thr Pro Thr Val Pro His Cys Ser Leu Ala Thr Leu Ile

85

90

95

Gly Leu Cys Leu Arg Val Lys Leu Gln Arg Cys Leu Pro Phe Lys His
 100 105 110

Lys Leu Glu Ile Tyr Ile Ser Glu Gly Thr His Ser Thr Glu Glu Asp
 115 120 125

Ile Asn Lys Gln Ile Asn Asp Lys Glu Arg Val Ala Ala Ala Met Glu
 130 135 140

Asn Pro Asn Leu Arg Glu Ile Val Glu Gln Cys Val Leu Glu Pro Asp
 145 150 155 160

<210> 25

<211> 2026

<212> DNA

<213> Homo sapiens

<400> 25

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<210> 26

<211> 354

<212> PRT

<213> Homo sapiens

<400> 26
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 Ile Gln Glu Glu Leu Gln Arg Ser Gly Gly Leu Asp His Leu Val Leu
 35 40 45
 Ser Pro Gly Glu Trp Pro Val Ser Asp Asn Thr Ile Met His Ile Ala
 50 55 60
 Thr Ala Glu Ala Leu Thr Thr Asp Tyr Trp Cys Leu Asp Asp Leu Tyr
 65 70 75 80
 Arg Glu Met Val Arg Cys Tyr Val Glu Ile Val Glu Lys Leu Pro Glu
 85 90 95
 Arg Arg Pro Asp Pro Ala Thr Ile Glu Gly Cys Ala Gln Leu Lys Pro
 100 105 110
 Asn Asn Tyr Leu Leu Ala Trp His Thr Pro Phe Asn Glu Lys Gly Ser
 115 120 125
 Gly Phe Gly Ala Ala Thr Lys Ala Met Cys Ile Gly Leu Arg Tyr Trp
 130 135 140
 Lys Pro Glu Arg Leu Glu Thr Leu Ile Glu Val Ser Val Glu Cys Gly
 145 150 155 160
 Arg Met Thr His Asn His Pro Thr Gly Phe Leu Gly Ser Leu Cys Thr
 165 170 175
 Ala Leu Phe Val Ser Phe Ala Ala Gln Gly Lys Pro Leu Val Gln Trp
 180 185 190
 Gly Arg Asp Met Leu Arg Ala Val Pro Leu Ala Glu Glu Tyr Cys Arg
 195 200 205
 Lys Thr Ile Arg His Thr Ala Glu Tyr Gln Glu His Trp Phe Tyr Phe
 210 215 220
 Glu Ala Lys Trp Gln Phe Tyr Leu Glu Glu Arg Lys Ile Ser Lys Asp
 225 230 235 240
 Ser Glu Asn Lys Ala Ile Phe Pro Asp Asn Tyr Asp Ala Glu Glu Arg
 245 250 255
 Glu Lys Thr Tyr Arg Lys Trp Ser Ser Glu Gly Arg Gly Gly Arg Arg
 260 265 270
 Gly His Asp Ala Pro Met Ile Ala Tyr Asp Ala Leu Leu Ala Ala Gly
 275 280 285
 Asn Ser Trp Thr Glu Leu Cys His Arg Ala Met Phe His Gly Gly Glu
 290 295 300
 Ser Ala Ala Thr Gly Thr Ile Ala Gly Cys Leu Phe Gly Leu Leu Tyr

305

310

315

320

Gly Leu Asp Leu Val Pro Lys Gly Leu Tyr Gln Asp Leu Glu Asp Lys
325 330 335

Glu Lys Leu Glu Asp Leu Gly Ala Ala Leu Tyr Arg Leu Ser Thr Glu
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Glu Lys

<210> 27

<211> 2512

<212> DNA

<213> Homo sapiens

<400> 27

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<210> 28
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 28
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 Gln Asn Leu Pro Ala Ser Val Leu Glu Val Asn Ala Ser Gln Thr His
 35 40 45
 Arg Gln Thr Thr Pro Glu Ala Ser Pro Pro Cys Pro Pro Ser Val Val
 50 55 60
 Pro Leu Asn Arg Ala Thr Phe Ser Pro Gly Ser Gly Thr Ser Ser Ala
 65 70 75 80
 Ser Leu Ser Leu Pro Pro Pro Asp Gly Val Gly Ser Ser Arg Leu His
 85 90 95
 Asn Pro Gln Ser Leu Ser His Cys Leu Tyr Lys His Leu Leu Pro Ala
 100 105 110
 Pro Glu Ser Leu Ile His Ser His Asp Thr Gly Ser Leu Thr Thr Asp
 115 120 125
 Ser Ser Leu Ala Glu His Ser Ser Arg Ser Glu Ser Glu Ser Ser Thr
 130 135 140
 Ala Met Leu Glu Glu Leu Gln Ile Gly Asp Ser Asp Thr Thr Gly Arg
 145 150 155 160
 Ser Glu Thr Pro Ser Pro Thr Trp Gly Gln Arg Ser Ala Val Thr Asp
 165 170 175
 Gly Thr Thr Leu Thr Thr Pro Ala Ala Thr His Val Ile Ile Leu Pro
 180 185 190
 Phe Phe Ala Ser Thr Val Ser Leu Lys Gly Leu Ile Cys Cys Ala Ile
 195 200 205

Ser Phe Phe Gly
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<210> 29
 <211> 1495
 <212> DNA
 <213> Homo sapiens

<400> 29
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<210> 30

<211> 72

<212> PRT

<213> Homo sapiens

<400> 30

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Met Leu Arg Pro Ala Leu Pro Trp Leu Cys Leu Gly Leu Cys Ser Leu
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```

Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
          20                      25                      30

```

```

Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
      35                      40                      45

```

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Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
    50                      55                      60

```

```

Val Tyr Lys Pro Ile Arg Arg Arg
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<210> 31

<211> 2714

<212> DNA

<213> Homo sapiens

<400> 31

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cttgccctaca tcatcaaaaag tgaatgcaac tgtaccaagt aatatgatgt cagttaatgg 180
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cttttgggaa tttgccacag acaattatga cattgggttt ggggtgtatt ttgaatggac 480
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2714

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<210> 32
 <211> 240
 <212> PRT
 <213> Homo sapiens

<400> 32
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 20 25 30
 Ser Lys Val Asn Ala Thr Val Pro Ser Asn Met Met Ser Val Asn Gly
 35 40 45
 Gln Ala Lys Thr His Thr Asp Ser Ser Glu Lys Glu Leu Glu Pro Glu
 50 55 60
 Ala Ala Glu Glu Ala Leu Glu Asn Gly Pro Lys Glu Ser Leu Pro Val
 65 70 75 80
 Ile Ala Ala Pro Ser Met Trp Thr Arg Pro Gln Ile Lys Asp Phe Lys
 85 90 95

.Glu Lys Ile Gln Gln Asp Ala Asp Ser Val Ile Thr Val Gly Arg Gly
 100 105 110
 Glu Val Val Thr Val Arg Val Pro Thr His Glu Glu Gly Ser Tyr Leu
 115 120 125
 Phe Trp Glu Phe Ala Thr Asp Asn Tyr Asp Ile Gly Phe Gly Val Tyr
 130 135 140
 Phe Glu Trp Thr Asp Ser Pro Asn Thr Ala Val Ser Val His Val Ser
 145 150 155 160
 Glu Ser Ser Asp Asp Asp Glu Glu Glu Glu Glu Asn Ile Gly Cys Glu
 165 170 175
 Glu Lys Ala Lys Lys Asn Ala Asn Lys Pro Leu Leu Asp Glu Ile Val
 180 185 190
 Pro Val Tyr Arg Arg Asp Cys His Glu Glu Val Tyr Ala Gly Ser His
 195 200 205
 Gln Tyr Pro Gly Arg Gly Val Tyr Leu Leu Lys Phe Asp Asn Ser Tyr
 210 215 220
 Ser Leu Trp Arg Ser Lys Ser Val Tyr Tyr Arg Val Tyr Tyr Thr Arg
 225 230 235 240

<210> 33

<211> 1136

<212> DNA

<213> Homo sapiens

<400> 33

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<210> 34

<211> 57

<212> PRT

<213> Homo sapiens

<400> 34

Met Val Lys Ala Val Ala Pro Asp Leu Phe Ala His Gln Leu Leu Leu
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Trp Ser Leu Arg Leu Leu Met Pro Ala Trp Leu Val Leu Ser Lys Lys
20 25 30

Val Lys Phe Asn Gln Arg Gly Asp Ala Asp Ala Phe Gln Tyr Leu Asn
35 40 45

Met Ser Ser Asp Pro Gly Ala Trp Thr
50 55

<210> 35

<211> 1394

<212> DNA

<213> Homo sapiens

<400> 35

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<210> 36

<211> 361

<212> PRT

<213> Homo sapiens

<400> 36

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20 25 30

Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val
35 40 45

Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly
 50 55 60
 Val Arg Val Leu Glu Glu Gln Leu Lys Ser Val Arg Glu Lys Trp Ala
 65 70 75 80
 Gln Glu Pro Leu Leu Gln Pro Leu Ser Leu Arg Val Gly Met Leu Gly
 85 90 95
 Glu Lys Leu Glu Ala Ala Ile Gln Arg Ser Leu His Tyr Leu Lys Leu
 100 105 110
 Ser Asp Pro Lys Tyr Ile Arg Glu Phe Gln Leu Thr Leu Gln Pro Gly
 115 120 125
 Phe Trp Lys Leu Pro His Ala Trp Ile His Thr Asp Ala Ser Leu Val
 130 135 140
 Tyr Pro Thr Phe Gly Pro Gln Asp Ser Phe Ser Glu Glu Arg Ser Asp
 145 150 155 160
 Val Cys Leu Val Gln Leu Leu Gly Thr Gly Thr Asp Ser Ser Glu Pro
 165 170 175
 Cys Gly Leu Ser Asp Leu Cys Arg Ser Leu Met Thr Lys Pro Gly Cys
 180 185 190
 Ser Gly Tyr Cys Leu Ser His Gln Leu Leu Phe Phe Leu Trp Ala Arg
 195 200 205
 Met Arg Gly Cys Thr Gln Gly Pro Leu Gln Gln Ser Gln Asp Tyr Ile
 210 215 220
 Asn Leu Phe Cys Ala Asn Met Met Asp Leu Asn Arg Arg Ala Glu Ala
 225 230 235 240
 Ile Gly Tyr Ala Tyr Pro Thr Arg Asp Ile Phe Met Glu Asn Ile Met
 245 250 255
 Phe Cys Gly Met Gly Gly Phe Ser Asp Phe Tyr Lys Leu Arg Trp Leu
 260 265 270
 Glu Ala Ile Leu Ser Trp Gln Lys Gln Gln Glu Gly Cys Phe Gly Glu
 275 280 285
 Pro Asp Ala Glu Asp Glu Glu Leu Ser Lys Ala Ile Gln Tyr Gln Gln
 290 295 300
 His Phe Ser Arg Arg Val Lys Arg Arg Glu Lys Gln Phe Pro Asp Gly
 305 310 315 320
 Cys Ser Ser His Asn Thr Ala Thr Ala Val Ala Ala Leu Gly Gly Phe
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 Leu Tyr Ile Leu Ala Glu Tyr Pro Pro Ala Asn Arg Glu Pro His Pro
 340 345 350
 Ser Thr Pro Pro Pro Pro Ser Ser Arg
 355 360

<210> 37
 <211> 1138
 <212> DNA
 <213> Homo sapiens

<400> 37
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<210> 38
 <211> 291
 <212> PRT
 <213> Homo sapiens

<400> 38
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 Cys Arg Asp Arg Leu Leu Gly His Arg Glu Pro Ser Ala His Pro Val
 20 25 30
 Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser Lys Glu Arg Val
 35 40 45
 Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala Thr Leu Leu Ile
 50 55 60
 Leu Asp Ile Cys Glu Asp Asn Val Pro Asp Pro Lys Asp Val Lys Glu
 65 70 75 80
 Arg Phe Ser Gly Ser Leu Val Ala Ala Leu Ser Ala Thr Gly Pro Arg
 85 90 95
 Phe Leu Ala Tyr Phe Gly Ser Phe Ala Thr Val Gly Leu Leu Trp Phe
 100 105 110
 Ala His His Ser Leu Phe Leu His Val Arg Lys Ala Thr Arg Ala Met
 115 120 125
 Gly Leu Leu Asn Thr Leu Ser Leu Ala Phe Val Gly Gly Leu Pro Leu
 130 135 140

Ala Tyr Gln Gln Thr Ser Ala Phe Ala Arg Gln Pro Arg Asp Glu Leu
 145 150 155 160

Glu Arg Val Arg Val Ser Cys Thr Ile Ile Phe Leu Ala Ser Ile Phe
 165 170 175

Gln Leu Ala Thr Trp Thr Thr Ala Leu Leu His Gln Ala Glu Thr Leu
 180 185 190

Gln Pro Ser Val Trp Phe Gly Gly Arg Glu His Val Leu Met Phe Ala
 195 200 205

Lys Leu Ala Leu Tyr Pro Cys Ala Ser Leu Leu Ala Phe Ala Ser Thr
 210 215 220

Cys Leu Leu Ser Arg Phe Ser Val Gly Ile Phe His Leu Met Glu Ile
 225 230 235 240

Ala Val Pro Cys Ala Phe Leu Leu Leu Arg Leu Leu Val Gly Leu Ala
 245 250 255

Leu Ala Thr Leu Arg Val Leu Arg Gly Leu Ala Arg Pro Glu His Pro
 260 265 270

Pro Pro Ala Pro Thr Gly Gln Asp Asp Pro Gln Ser Gln Leu Leu Pro
 275 280 285

Ala Pro Cys
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<210> 39
 <211> 1478
 <212> DNA
 <213> Homo sapiens

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<210> 40
 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 40

Met Thr Gln Asn Thr Val Ile Val Asn Gly Val Ala Met Ala Ser Arg
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Pro Ser Gln Pro Thr His Val Asn Val His Ile His Gln Glu Ser Ala
 20 25 30

Leu Thr Gln Leu Leu Lys Ala Gly Gly Ser Leu Lys Lys Phe Leu Phe
 35 40 45

His Pro Gly Asp Thr Val Pro Ser Thr Ala Arg Ile Gly Tyr Glu Gln
 50 55 60

Leu Ala Leu Gly Val Thr Gln Ile Leu Leu Gly Val Val Ser Cys Val
 65 70 75 80

Leu Gly Val Cys Leu Ser Leu Gly Pro Trp Thr Val Leu Ser Ala Ser
 85 90 95

Gly Cys Ala Phe Trp Ala Gly Ser Val Val Ile Ala Ala Gly Ala Gly
 100 105 110

Ala Ile Val His Glu Lys His Pro Gly Lys Leu Ala Gly Tyr Ile Ser
 115 120 125

Ser Leu Leu Thr Leu Ala Gly Phe Ala Thr Ala Met Ala Ala Val Val
 130 135 140

Leu Cys Val Asn Ser Phe Ile Trp Gln Thr Glu Pro Phe Leu Tyr Ile
 145 150 155 160

Asp Thr Val Cys Asp Arg Ser Asp Pro Val Phe Pro Thr Thr Gly Tyr
 165 170 175

Arg Trp Met Arg Arg Ser Gln Glu Asn Gln Trp Gln Lys Glu Glu Cys
 180 185 190

Arg Ala Tyr Met Gln Met Leu Arg Lys Leu Phe Thr Ala Ile Arg Ala
 195 200 205

Leu Phe Leu Ala Val Cys Val Leu Lys Val Ile Val Ser Leu Val Ser
 210 215 220

Leu Gly Val Gly Leu Arg Asn Leu Phe Gly Gln Ser Ser Gln Pro Leu
 225 230 235 240

Asn Glu Glu Gly Ser Glu Lys Arg Leu Leu Gly Glu Asn Ser Val Pro
 245 250 255

Pro Ser Pro Ser Arg Glu Gln Thr Ser Thr Ala Ile Val Leu
 260 265 270

<210> 41
<211> 2828
<212> DNA
<213> Homo sapiens

<400> 41
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<210> 42
<211> 124
<212> PRT
<213> Homo sapiens

<400> 42

Met Pro Pro Asn Val Glu Leu Val Val His Cys Leu Gly Leu Trp Pro
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Ser His Pro Ala Val Glu Ala Glu Val Glu Asp Glu Ala Ser Gln Glu
 20 25 30

Gly Asp Phe Ser His Ser Ser His Ala Ser Ala Leu Tyr Leu Phe Ser
 35 40 45

Lys Ala Gln Leu Arg Cys Ala Gly Trp Ser Cys Leu Ala Val Ile Leu
 50 55 60

Ala Phe Trp Leu Met Val Gln Ser Ser Ser Leu Ala Asp Pro Leu Phe
 65 70 75 80

Leu Leu Cys Phe Arg Gly Asn Pro Gly Asn Ala Leu Thr Ala Arg Leu
 85 90 95

Ser Leu His Pro Cys Trp Leu Val Leu Ala Arg Leu Arg Gly Pro Pro
 100 105 110

Leu Phe Leu Ala Arg Ser Tyr Leu Thr Phe Asp Val
 115 120

<210> 43

<211> 646

<212> DNA

<213> Homo sapiens

<400> 43

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<210> 44

<211> 111

<212> PRT

<213> Homo sapiens

<400> 44

Met Gly Ser Thr Trp Gly Ser Pro Gly Trp Val Arg Leu Ala Leu Cys
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Leu Thr Gly Leu Val Leu Ser Leu Tyr Ala Leu His Val Lys Ala Ala
 20 25 30

Arg Ala Arg Asp Arg Asp Tyr Arg Ala Leu Cys Asp Val Gly Thr Ala
 35 40 45

Ile Ser Cys Ser Arg Val Phe Ser Ser Arg Trp Gly Arg Gly Phe Gly
 50 55 60

Leu Val Glu His Val Leu Gly Gln Asp Ser Ile Leu Asn Gln Ser Asn
 65 70 75 80

Ser Ile Phe Gly Cys Ile Phe Tyr Thr Leu Gln Leu Leu Leu Gly Cys
 85 90 95

Leu Arg Thr Arg Trp Ala Ser Val Leu Met Leu Leu Ser Leu Ala
 100 105 110

<210> 45
 <211> 1612
 <212> DNA
 <213> Homo sapiens

<400> 45
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<210> 46
 <211> 372
 <212> PRT
 <213> Homo sapiens

<400> 46
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 20 25 30

Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn

35	40	45
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Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser 65 70 75 80		
Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp 85 90 95		
Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp 100 105 110		
Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu 115 120 125		
Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln 130 135 140		
Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val 145 150 155 160		
Ile Leu Lys Ser Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His 165 170 175		
Trp Gly Leu Tyr Ile Phe Ser Leu Ala Gln Leu Phe Tyr Thr Thr Val 180 185 190		
Leu Val Leu Cys Tyr Val Ile Tyr Phe Thr Lys Leu Leu Gly Ser Pro 195 200 205		
Glu Ser Thr Lys Leu Gln Thr Leu Pro Val Ser Arg Ile Thr Asp Leu 210 215 220		
Leu Pro Asn Ile Thr Arg Asn Gly Ala Phe Ile Asn Trp Lys Glu Ala 225 230 235 240		
Lys Leu Thr Trp Ser Phe Phe Lys Gln Ser Phe Leu Lys Gln Ile Leu 245 250 255		
Thr Glu Gly Glu Arg Tyr Val Met Thr Phe Leu Asn Val Leu Asn Phe 260 265 270		
Gly Asp Gln Gly Val Tyr Asp Ile Val Asn Asn Leu Gly Ser Leu Val 275 280 285		
Ala Arg Leu Ile Phe Gln Pro Ile Glu Glu Ser Phe Tyr Ile Phe Phe 290 295 300		
Ala Lys Val Leu Glu Arg Gly Lys Asp Ala Thr Leu Gln Lys Gln Glu 305 310 315 320		
Asp Val Ala Val Ala Ala Ala Val Leu Glu Ser Leu Leu Lys Leu Ala 325 330 335		
Leu Leu Ala Gly Leu Thr Ile Thr Val Phe Gly Phe Ala Tyr Ser Gln 340 345 350		
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355

360

365

Ile Pro Leu Leu
370

<210> 47
<211> 3094
<212> DNA
<213> Homo sapiens

<400> 47

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<210> 48

<211> 464

<212> PRT

<213> Homo sapiens

<400> 48

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Gly Tyr Pro Glu Pro Tyr Gly Lys Gly Gln Glu Ser Ser Thr Asp Ile
35 40 45

Lys Ala Pro Glu Gly Phe Ala Val Arg Leu Val Phe Gln Asp Phe Asp
50 55 60

Leu Glu Pro Ser Gln Asp Cys Ala Gly Asp Ser Val Thr Ile Ser Phe
65 70 75 80

Val Gly Ser Asp Pro Ser Gln Phe Cys Gly Gln Gln Gly Ser Pro Leu
85 90 95

Gly Arg Pro Pro Gly Gln Arg Glu Phe Val Ser Ser Gly Arg Ser Leu
100 105 110

Arg Leu Thr Phe Arg Thr Gln Pro Ser Ser Glu Asn Lys Thr Ala His
115 120 125

Leu His Lys Gly Phe Leu Ala Leu Tyr Gln Thr Val Ala Val Asn Tyr
130 135 140

Ser Gln Pro Ile Ser Glu Ala Ser Arg Gly Ser Glu Ala Ile Asn Ala
145 150 155 160

Pro Gly Asp Asn Pro Ala Lys Val Gln Asn His Cys Gln Glu Pro Tyr
165 170 175

Tyr Gln Ala Ala Ala Ala Gly Ala Leu Thr Cys Ala Thr Pro Gly Thr
180 185 190

Trp Lys Asp Arg Gln Asp Gly Glu Glu Val Leu Gln Cys Met Pro Val
195 200 205

Cys Gly Arg Pro Val Thr Pro Ile Ala Gln Asn Gln Thr Thr Leu Gly
210 215 220

Ser Ser Arg Ala Lys Leu Gly Asn Phe Pro Trp Gln Ala Phe Thr Ser
225 230 235 240

Ile His Gly Arg Gly Gly Gly Ala Leu Leu Gly Asp Arg Trp Ile Leu
245 250 255

Thr Ala Ala His Thr Val Tyr Pro Lys Asp Ser Val Ser Leu Arg Lys

260 265 270
 Asn Gln Ser Val Asn Val Phe Leu Gly His Thr Ala Ile Asp Glu Met
 275 280 285
 Leu Lys Leu Gly Asn His Pro Val His Arg Val Val Val His Pro Asp
 290 295 300
 Tyr Arg Gln Asn Glu Ser His Asn Phe Ser Gly Asp Ile Ala Leu Leu
 305 310 315 320
 Glu Leu Gln His Ser Ile Pro Leu Gly Pro Asn Val Leu Pro Val Cys
 325 330 335
 Leu Pro Asp Asn Glu Thr Leu Tyr Arg Ser Gly Leu Leu Gly Tyr Val
 340 345 350
 Ser Gly Phe Gly Met Glu Met Gly Trp Leu Thr Thr Glu Leu Lys Tyr
 355 360 365
 Ser Arg Leu Pro Val Ala Pro Arg Glu Ala Cys Asn Ala Trp Leu Gln
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 Lys Arg Gln Arg Pro Glu Val Phe Ser Asp Asn Met Phe Cys Val Gly
 385 390 395 400
 Asp Glu Thr Gln Arg His Ser Val Cys Gln Gly Asp Ser Gly Ser Val
 405 410 415
 Tyr Val Val Trp Asp Asn His Ala His His Trp Val Ala Thr Gly Ile
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 Val Ser Trp Gly Ile Gly Cys Gly Glu Gly Tyr Asp Phe Tyr Thr Lys
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<210> 49

<211> 2927

<212> DNA

<213> Homo sapiens

<400> 49

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<210> 50

<211> 627

<212> PRT

<213> Homo sapiens

<400> 50

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Met Gly Leu Leu Gln Gly Leu Leu Arg Val Arg Lys Leu Leu Leu Val
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Val Cys Val Pro Leu Leu Leu Leu Pro Leu Pro Val Leu His Pro Ser
      20                      25          30

```

```

Ser Glu Ala Ser Cys Ala Tyr Val Leu Ile Val Thr Ala Val Tyr Trp
      35                      40          45

```

```

Val Ser Glu Ala Val Pro Leu Gly Ala Ala Ala Leu Val Pro Ala Phe
      50                      55          60

```

```

Leu Tyr Pro Phe Phe Gly Val Leu Arg Ser Asn Glu Val Ala Ala Glu
      65                      70          75          80

```

```

Tyr Phe Lys Asn Thr Thr Leu Leu Leu Val Gly Val Ile Cys Val Ala
      85                      90          95

```

```

Ala Ala Val Glu Lys Trp Asn Leu His Lys Arg Ile Ala Leu Arg Met

```

100	105	110
Val Leu Met Ala Gly Ala Lys	Pro Gly Met Leu Leu Leu Cys Phe Met	
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Cys Cys Thr Thr Leu Leu Ser Met Trp Leu Ser Asn Thr Ser Thr Thr		
130	135	140
Ala Met Val Met Pro Ile Val Glu Ala Val Leu Gln Glu Leu Val Ser		
145	150	155
Ala Glu Asp Glu Gln Leu Val Ala Gly Asn Ser Asn Thr Glu Glu Ala		
165	170	175
Glu Pro Ile Ser Leu Asp Val Lys Asn Ser Gln Pro Ser Leu Glu Leu		
180	185	190
Ile Phe Val Asn Glu Asp Arg Ser Asn Ala Asp Leu Thr Thr Leu Met		
195	200	205
His Asn Glu Asn Leu Asn Gly Val Pro Ser Ile Thr Asn Pro Ile Lys		
210	215	220
Thr Ala Asn Gln His Gln Gly Lys Lys Gln His Pro Ser Gln Glu Lys		
225	230	235
Pro Gln Val Leu Thr Pro Ser Pro Arg Lys Gln Lys Leu Asn Arg Lys		
245	250	255
Tyr Arg Ser His His Asp Gln Met Ile Cys Lys Cys Leu Ser Leu Ser		
260	265	270
Ile Ser Tyr Ser Ala Thr Ile Gly Gly Leu Thr Thr Ile Ile Gly Thr		
275	280	285
Ser Thr Ser Leu Ile Phe Leu Glu His Phe Asn Asn Gln Tyr Pro Ala		
290	295	300
Ala Glu Val Val Asn Phe Gly Thr Trp Phe Leu Phe Ser Phe Pro Ile		
305	310	315
Ser Leu Ile Met Leu Val Val Ser Trp Phe Trp Met His Trp Leu Phe		
325	330	335
Leu Gly Cys Asn Phe Lys Glu Thr Cys Ser Leu Ser Lys Lys Lys Lys		
340	345	350
Thr Lys Arg Glu Gln Leu Ser Glu Lys Arg Ile Gln Glu Glu Tyr Glu		
355	360	365
Lys Leu Gly Asp Ile Ser Tyr Pro Glu Met Val Thr Gly Phe Phe Phe		
370	375	380
Ile Leu Met Thr Val Leu Trp Phe Thr Arg Glu Pro Gly Phe Val Pro		
385	390	395
Gly Trp Asp Ser Phe Phe Glu Lys Lys Gly Tyr Arg Thr Asp Ala Thr		
405	410	415
Val Ser Val Phe Leu Gly Phe Leu Leu Phe Leu Ile Pro Ala Lys Lys		

420 425 430
 Pro Cys Phe Gly Lys Lys Asn Asp Gly Glu Asn Gln Glu His Ser Leu
 435 440 445
 Gly Thr Glu Pro Ile Ile Thr Trp Lys Asp Phe Gln Lys Thr Met Pro
 450 455 460
 Trp Glu Ile Val Ile Leu Val Gly Gly Gly Tyr Ala Leu Ala Ser Gly
 465 470 475 480
 Ser Lys Ser Ser Gly Leu Ser Thr Trp Ile Gly Asn Gln Met Leu Ser
 485 490 495
 Leu Ser Ser Leu Pro Pro Trp Ala Val Thr Leu Leu Ala Cys Ile Leu
 500 505 510
 Val Ser Ile Val Thr Glu Phe Val Ser Asn Pro Ala Thr Ile Thr Ile
 515 520 525
 Phe Leu Pro Ile Leu Cys Ser Leu Ser Glu Thr Leu His Ile Asn Pro
 530 535 540
 Leu Tyr Thr Leu Ile Pro Val Thr Met Cys Ile Ser Phe Ala Val Met
 545 550 555 560
 Leu Pro Val Gly Asn Pro Pro Asn Ala Ile Val Phe Ser Tyr Gly His
 565 570 575
 Cys Gln Ile Lys Asp Met Val Lys Ala Gly Leu Gly Val Asn Val Ile
 580 585 590
 Gly Leu Val Ile Val Met Val Ala Ile Asn Thr Trp Gly Val Ser Leu
 595 600 605
 Phe His Leu Asp Thr Tyr Pro Ala Trp Ala Arg Val Ser Asn Ile Thr
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 Asp Gln Ala
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<210> 51

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 51

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa                                     2134

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<210> 52

<211> 540

<212> PRT

<213> Homo sapiens

<400> 52

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Met Ala Thr Ser Gly Ala Ala Ser Ala Glu Leu Val Ile Gly Trp Cys
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Ile Phe Gly Leu Leu Leu Ala Ile Leu Ala Phe Cys Trp Ile Tyr
      20              25              30

```

```

Val Arg Lys Tyr Gln Ser Arg Arg Glu Ser Glu Val Val Ser Thr Ile
      35              40              45

```

```

Thr Ala Ile Phe Ser Leu Ala Ile Ala Leu Ile Thr Ser Ala Leu Leu
      50              55              60

```

```

Pro Val Asp Ile Phe Leu Val Ser Tyr Met Lys Asn Gln Asn Gly Thr
      65              70              75              80

```

```

Phe Lys Asp Trp Ala Asn Ala Asn Val Ser Arg Gln Ile Glu Asp Thr
      85              90              95

```

```

Val Leu Tyr Gly Tyr Tyr Thr Leu Tyr Ser Val Ile Leu Phe Cys Val
      100             105             110

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```

Phe Phe Trp Ile Pro Phe Val Tyr Phe Tyr Tyr Glu Glu Lys Asp Asp
      115             120             125

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```

Asp Asp Thr Ser Lys Cys Thr Gln Ile Lys Thr Ala Leu Lys Tyr Thr
      130             135             140

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Leu Gly Phe Val Val Ile Cys Ala Leu Leu Leu Leu Val Gly Ala Phe
      145             150             155             160

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Val Pro Leu Asn Val Pro Asn Asn Lys Asn Ser Thr Glu Trp Glu Lys
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 Val Lys Ser Leu Phe Glu Glu Leu Gly Ser Ser His Gly Leu Ala Ala
 180 185 190
 Leu Ser Phe Ser Ile Ser Ser Leu Thr Leu Ile Gly Met Leu Ala Ala
 195 200 205
 Ile Thr Tyr Thr Ala Tyr Gly Met Ser Ala Leu Pro Leu Asn Leu Ile
 210 215 220
 Lys Gly Thr Arg Ser Ala Ala Tyr Glu Arg Leu Glu Asn Thr Glu Asp
 225 230 235 240
 Ile Glu Glu Val Glu Gln His Ile Gln Thr Ile Lys Ser Lys Ser Lys
 245 250 255
 Asp Gly Arg Pro Leu Pro Ala Arg Asp Lys Arg Ala Leu Lys Gln Phe
 260 265 270
 Glu Glu Arg Leu Arg Thr Leu Lys Lys Arg Glu Arg His Leu Glu Phe
 275 280 285
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 290 295 300
 Lys Ile Val Trp Gly Ile Phe Phe Ile Leu Val Ala Leu Leu Phe Val
 305 310 315 320
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 325 330 335
 Ile Asp Ser Gly Phe Ile Ile Phe Gly Ala Asn Leu Ser Asn Pro Leu
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 Asn Met Leu Leu Pro Leu Leu Gln Thr Val Phe Pro Leu Asp Tyr Ile
 355 360 365
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 370 375 380
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 385 390 395 400
 Arg Arg Gly Arg Thr Arg Pro Gln Ala Leu Leu Phe Leu Cys Met Ile
 405 410 415
 Leu Leu Leu Ile Val Leu His Thr Ser Tyr Met Ile Tyr Ser Leu Ala
 420 425 430
 Pro Gln Tyr Val Met Tyr Gly Ser Gln Asn Tyr Leu Ile Glu Thr Asn
 435 440 445
 Ile Thr Ser Asp Asn His Lys Gly Asn Ser Thr Leu Ser Val Pro Lys
 450 455 460
 Arg Cys Asp Ala Glu Ala Pro Glu Asp Gln Cys Thr Val Thr Arg Thr
 465 470 475 480

Tyr Leu Phe Leu His Lys Phe Trp Phe Phe Ser Ala Ala Tyr Tyr Phe
485 490 495

Gly Asn Trp Ala Phe Leu Gly Val Phe Leu Ile Gly Leu Ile Val Ser
500 505 510

Cys Cys Lys Gly Lys Lys Ser Val Ile Glu Gly Val Asp Glu Asp Ser
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Asp Ile Ser Asp Asp Glu Pro Ser Val Tyr Ser Ala
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<210> 53

<211> 1987

<212> DNA

<213> Homo sapiens

<400> 53

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cttcttcaca taatttgccg gtgttctttt tacagagcaa ttatcttgta tatacaactt 1860
tgtatcctgc cttttccacc ttatcggttc atcactttat tccagcactt ctctgtgttt 1920
tacagacctt ttataaata aaatgttcat cagctgcata ttccaaaaaa aaaaaaaaaa 1980
aaaaaaa 1987

<210> 54

<211> 79

<212> PRT

<213> Homo sapiens

<400> 54

Met Asp Gly Gly Leu Glu Leu Val Glu Lys Ala Gly Trp Thr Gln Gln
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Leu Pro Gly Asp His Pro Ser His Leu Pro Pro Leu His Leu Gly Ser
 20 25 30

Ala Leu Gln Thr Pro Leu Leu Ser Leu Gln Thr Ala Glu Lys Glu
 35 40 45

Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro Pro Leu
 50 55 60

His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val Ser Ala
 65 70 75

<210> 55

<211> 1747

<212> DNA

<213> Homo sapiens

<400> 55

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 aataatctca ttgaagaatg tgaacaagct gaacgacttg gagcagtggg tgaatctctg 480
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 ttctgtgaag ctgatgacat tcagtcacct gaagctgaat atgtagattt gcttcttaac 600
 cctgagcgct acactggtta caagggacca gatgcttggg aaatatggaa tgtcatctac 660
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 agagtggaaat ttcatcctaaa ggcataatag caatgacagt cttaagccaa acattttata 1560
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 tgttaagtct atgtataata ctactgtgag taaaagtaat actttaataa tgtggtacaa 1680
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 aaaaaaa 1747

<210> 56

<211> 468

<212> PRT

<213> Homo sapiens

<400> 56

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 20 25 30
 Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp Cys Thr Cys
 35 40 45
 Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg Leu Phe Pro Arg
 50 55 60
 Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg Tyr Tyr Lys Val Asn
 65 70 75 80
 Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp Ile Ser Gln Cys Gly Arg
 85 90 95
 Arg Asp Cys Ala Val Lys Pro Cys Gln Ser Asp Glu Val Pro Asp Gly
 100 105 110
 Ile Lys Ser Ala Ser Tyr Lys Tyr Ser Glu Glu Ala Asn Asn Leu Ile
 115 120 125
 Glu Glu Cys Glu Gln Ala Glu Arg Leu Gly Ala Val Asp Glu Ser Leu
 130 135 140
 Ser Glu Glu Thr Gln Lys Ala Val Leu Gln Trp Thr Lys His Asp Asp
 145 150 155 160
 Ser Ser Asp Asn Phe Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala
 165 170 175
 Glu Tyr Val Asp Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys
 180 185 190
 Gly Pro Asp Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys
 195 200 205
 Phe Lys Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly
 210 215 220
 Gln Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu
 225 230 235 240
 Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His Ala
 245 250 255
 Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu Thr Trp
 260 265 270
 Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln Gln Arg Phe
 275 280 285
 Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg Leu Lys Asn Leu
 290 295 300
 Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu Ser Lys Val Leu Pro
 305 310 315 320

Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe Thr Gly Asn Lys Ile Gln
 325 330 335
 Asp Glu Glu Asn Lys Met Leu Leu Leu Glu Ile Leu His Glu Ile Lys
 340 345 350
 Ser Phe Pro Leu His Phe Asp Glu Asn Ser Phe Phe Ala Gly Asp Lys
 355 360 365
 Lys Glu Ala His Lys Leu Lys Glu Asp Phe Arg Leu His Phe Arg Asn
 370 375 380
 Ile Ser Arg Ile Met Asp Cys Val Gly Cys Phe Lys Cys Arg Leu Trp
 385 390 395 400
 Gly Lys Leu Gln Thr Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe
 405 410 415
 Ser Glu Lys Leu Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu
 420 425 430
 Phe His Leu Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly
 435 440 445
 Arg Ile Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu
 450 455 460
 Gln Asn Ile His
 465

<210> 57
 <211> 1293
 <212> DNA
 <213> Homo sapiens

<400> 57
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 cgccgggggt cagcgcgatc tcctgcaccg tcgagggggc acccgccagc tttggcaaga 180
 gcttcgcgca gaaatctggc tacttctgt gccttagttc tctgggcagc ctagagaacc 240
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 gcttctcccc cgtctgcgac cccatggatt ccaaggccctc tgtgtccaag aagaaacgca 360
 tgtgtgtgaa gctgttgccc ctgggagcca cggacacggc tgtgtttgat gtccggctga 420
 gtgggaagac caagacagt cctggatacc ttcgaaatagg ggacatgggc ggctttgcca 480
 tctggtgcaa gaaggccaag gccccgaggc cagtgcceaa gccccgaggt ctcagccggg 540
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<210> 58
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 58

Met Asp Pro Val Pro Gly Thr Asp Ser Ala Pro Leu Ala Gly Leu Ala
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 Trp Ser Ser Ala Ser Ala Pro Pro Pro Arg Gly Phe Ser Ala Ile Ser
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 Cys Thr Val Glu Gly Ala Pro Ala Ser Phe Gly Lys Ser Phe Ala Gln
 35 40 45
 Lys Ser Gly Tyr Phe Leu Cys Leu Ser Ser Leu Gly Ser Leu Glu Asn
 50 55 60
 Pro Gln Glu Asn Val Val Ala Asp Ile Gln Ile Val Val Asp Lys Ser
 65 70 75 80
 Pro Leu Pro Leu Gly Phe Ser Pro Val Cys Asp Pro Met Asp Ser Lys
 85 90 95
 Ala Ser Val Ser Lys Lys Lys Arg Met Cys Val Lys Leu Leu Pro Leu
 100 105 110
 Gly Ala Thr Asp Thr Ala Val Phe Asp Val Arg Leu Ser Gly Lys Thr
 115 120 125
 Lys Thr Val Pro Gly Tyr Leu Arg Ile Gly Asp Met Gly Gly Phe Ala
 130 135 140
 Ile Trp Cys Lys Lys Ala Lys Ala Pro Arg Pro Val Pro Lys Pro Arg
 145 150 155 160
 Gly Leu Ser Arg Asp Met Gln Gly Leu Ser Leu Asp Ala Ala Ser Gln
 165 170 175
 Pro Ser Lys Gly Gly Leu Leu Glu Arg Thr Ala Ser Arg Leu Gly Ser
 180 185 190
 Arg Ala Ser Thr Leu Arg Arg Asn Asp Ser Ile Tyr Glu Ala Ser Ser
 195 200 205
 Leu Tyr Gly Ile Ser Ala Met Asp Gly Val Pro Phe Thr Leu His Pro
 210 215 220
 Arg Phe Glu Gly Lys Ser Cys Ser Pro Leu Ala Phe Ser Ala Phe Gly
 225 230 235 240
 Asp Leu Thr Ile Lys Ser Leu Ala Asp Ile Glu Glu Glu Tyr Asn Tyr
 245 250 255
 Gly Phe Val Val Glu Lys Thr Ala Ala Ala Arg Leu Pro Pro Ser Val
 260 265 270
 Ser

<210> 59
<211> 2941
<212> DNA
<213> Homo sapiens

<400> 59
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a 2941

<210> 60
<211> 92

<212> PRT

<213> Homo sapiens..

<400> 60

Met Ala Ala Ala Ala Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu
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Leu Leu Leu Phe Leu Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg
20 25 30
Ala Gly Pro Asp Glu Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala
35 40 45
Pro Ala Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu
50 55 60
Pro Ala Arg Val Glu Val Ser Gly Pro Gly Trp Gly Glu Arg Gly Cys
65 70 75 80
Arg Ala Gly Cys Ala Glu Tyr Gln Ala Pro Gly Leu
85 90

<210> 61

<211> 1996

<212> DNA

<213> Homo sapiens

<400> 61

actagattag tccagtgtaa gaggtagaca attcatgttg aattttctgg aattactgca 60
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agcaagtggg gagaccataa gtgaaaaggg gagagtgttg agcctgatcc taccctatgc 180
tgatgtctct tcttatgtct atttcaccag gagactctct gggggccagg cctgggcttc 240
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gctcagttag aagggccctg tattcacctc cactgcccc aggggctgtg gacaaaccgg 1860

ctgggggact gccagcctc ccacctgttt atttaactta tttcaagtgc tttataataa 1920
 aggaaacact aacaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
 aaaaaaaaaa aaaaaa 1996

<210> 62

<211> 482

<212> PRT

<213> Homo sapiens

<400> 62

Met Leu Met Ser Leu Leu Met Ser Ile Ser Pro Gly Asp Ser Leu Gly
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Ala Arg Pro Gly Leu Pro Tyr Gly Leu Ser Asp Asp Glu Ser Gly Gly
 20 25 30

Gly Arg Ala Leu Ser Ala Glu Ser Glu Val Glu Glu Pro Ala Arg Gly
 35 40 45

Pro Gly Glu Ala Arg Gly Glu Arg Pro Gly Pro Ala Cys Gln Leu Cys
 50 55 60

Gly Gly Pro Thr Gly Glu Gly Pro Cys Cys Gly Ala Gly Gly Pro Gly
 65 70 75 80

Gly Gly Pro Leu Leu Pro Pro Arg Leu Leu Tyr Ser Cys Arg Leu Cys
 85 90 95

Thr Phe Val Ser His Tyr Ser Ser His Leu Lys Arg His Met Gln Thr
 100 105 110

His Ser Gly Glu Lys Pro Phe Arg Cys Gly Arg Cys Pro Tyr Ala Ser
 115 120 125

Ala Gln Leu Val Asn Leu Thr Arg His Thr Arg Thr His Thr Gly Glu
 130 135 140

Lys Pro Tyr Arg Cys Pro His Cys Pro Phe Ala Cys Ser Ser Leu Gly
 145 150 155 160

Asn Leu Arg Arg His Gln Arg Thr His Ala Gly Pro Pro Thr Pro Pro
 165 170 175

Cys Pro Thr Cys Gly Phe Arg Cys Cys Thr Pro Arg Pro Ala Arg Pro
 180 185 190

Pro Ser Pro Thr Glu Gln Glu Gly Ala Val Pro Arg Arg Pro Glu Asp
 195 200 205

Ala Leu Leu Leu Pro Asp Leu Ser Leu His Val Pro Pro Gly Gly Ala
 210 215 220

Ser Phe Leu Pro Asp Cys Gly Gln Leu Arg Gly Glu Gly Glu Gly Leu
 225 230 235 240

Cys Gly Thr Gly Ser Glu Pro Leu Pro Glu Leu Leu Phe Pro Trp Thr
 245 250 255

Cys Arg Gly Cys Gly Gln Glu Leu Glu Glu Gly Glu Gly Ser Arg Leu
 260 265 270

Gly Ala Ala Met Cys Gly Arg Cys Met Arg Gly Glu Ala Gly Gly Gly
 275 280 285
 Ala Ser Gly Gly Pro Gln Gly Pro Ser Asp Lys Gly Phe Ala Cys Ser
 290 295 300
 Leu Cys Pro Phe Ala Thr His Tyr Pro Asn His Leu Ala Arg His Met
 305 310 315 320
 Lys Thr His Ser Gly Glu Lys Pro Phe Arg Cys Ala Arg Cys Pro Tyr
 325 330 335
 Ala Ser Ala His Leu Asp Asn Leu Lys Arg His Gln Arg Val His Thr
 340 345 350
 Gly Glu Lys Pro Tyr Lys Cys Pro Leu Cys Pro Tyr Ala Cys Gly Asn
 355 360 365
 Leu Ala Asn Leu Lys Arg His Gly Arg Ile His Ser Gly Asp Lys Pro
 370 375 380
 Phe Arg Cys Ser Leu Cys Asn Tyr Ser Cys Asn Gln Ser Met Asn Leu
 385 390 395 400
 Lys Arg His Met Leu Arg His Thr Gly Glu Lys Pro Phe Arg Cys Ala
 405 410 415
 Thr Cys Ala Tyr Thr Thr Gly His Trp Asp Asn Tyr Lys Arg His Gln
 420 425 430
 Lys Val His Gly His Gly Gly Ala Gly Gly Pro Gly Leu Ser Ala Ser
 435 440 445
 Glu Gly Trp Ala Pro Pro His Ser Pro Pro Ser Val Leu Ser Ser Arg
 450 455 460
 Gly Pro Pro Ala Leu Gly Thr Ala Gly Ser Arg Ala Val His Thr Asp
 465 470 475 480
 Ser Ser

<210> 63
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 63
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21

<210> 64
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 64
cgcagcaaaa cacagtagtg a

<210> 65
<211> 20
<212> DNA
<213> Artificial Sequence

21

<220>
<223> oligonucleotide

<400> 65
tataaccaggt gtgccagctg

<210> 66
<211> 20
<212> DNA
<213> Artificial Sequence

20

<220>
<223> oligonucleotide

<400> 66
ccaagcttcc cgtgtagtgt

<210> 67
<211> 20
<212> DNA
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20

<220>
<223> oligonucleotide

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agagagggtg tcctgagggt

<210> 68
<211> 20
<212> DNA
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20

<220>
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<400> 68
tctcagctcc atctcagggt

<210> 69
<211> 21
<212> DNA
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20

<220>
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<213> Homo sapiens

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20 25 30

Trp Val Pro Leu Leu Gln Met Leu Asp Gln Ser Pro Arg Arg Val Met
35 40 45

Arg Lys Ser Val Ser Gln Leu Cys Pro Leu Leu Arg Pro His Pro Pro
50 55 60

Leu Ser Ser Lys His Pro Leu Val Leu Pro Leu Gln Leu Pro Pro Thr
65 70 75 80

Phe Leu His Leu Leu Pro Gly Pro Gly Cys Pro Gly Gln Thr Val Ala
85 90 95

Tyr Trp Val Arg Thr Pro Pro Val Trp Cys Trp Arg Ile Leu Arg Arg
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Cys Gln Asp Gln Asn Arg Leu Trp Ile Ile Gly Val Met Gly Ser Thr
115 120 125

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<211> 77

<212> PRT

<213> Homo sapiens

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20

25

30

Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu Pro Pro Glu
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Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu His Ile His Tyr
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Thr Gly Ser Leu Val Met Asp Val Leu Leu Thr Pro Pro
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<211> 152

<212> PRT

<213> Homo sapiens

<400> 90

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 20 25 30

Pro Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly Leu Glu
 35 40 45

Gln Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala Ile Ile
 50 55 60

Pro Ser His Leu Ala Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val Pro
 65 70 75 80

Ala Asp Ala Val Val Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile Arg
 85 90 95

Ala Asn Tyr Trp Leu Lys Leu Val Lys Gly Ile Leu Pro Leu Val Gly
 100 105 110

Met Ala Met Val Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu Tyr
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Lys Arg Asn Lys Ser Lys Lys Lys
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<211> 398

<212> PRT

<213> Homo sapiens

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Leu Ala Ser His Leu Ser Thr Val Glu Ser Glu Lys Gln Lys Leu Arg
 20 25 30

Ala Gln Val Arg Arg Leu Cys Gln Glu Asn Gln Trp Leu Arg Asp Glu
 35 40 45

Leu Ala Gly Thr Gln Gln Arg Leu Gln Arg Ser Glu Gln Ala Val Ala
 50 55 60

Gln Leu Glu Glu Glu Lys Lys His Leu Glu Phe Leu Gly Gln Leu Arg
 65 70 75 80

Gln Tyr Asp Glu Asp Gly His Thr Ser Glu Glu Lys Glu Gly Asp Ala
 85 90 95

Thr Lys Asp Ser Leu Asp Asp Leu Phe Pro Asn Glu Glu Glu Glu Asp
 100 105 110

Pro Ser Asn Gly Leu Ser Arg Gly Gln Gly Ala Thr Ala Ala Gln Gln
 115 120 125

Gly Gly Tyr Glu Ile Pro Ala Arg Leu Arg Thr Leu His Asn Leu Val
 130 135 140

Ile Gln Tyr Ala Ala Gln Gly Arg Tyr Glu Val Ala Val Pro Leu Cys
 145 150 155 160

Lys Gln Ala Leu Glu Asp Leu Glu Arg Thr Ser Gly Arg Gly His Pro
 165 170 175

Asp Val Ala Thr Met Leu Asn Ile Leu Ala Leu Val Tyr Arg Asp Gln
 180 185 190

Asn Lys Tyr Lys Glu Ala Ala His Leu Leu Asn Asp Ala Leu Ser Ile
 195 200 205

Arg Glu Ser Thr Leu Gly Pro Asp His Pro Ala Val Ala Ala Thr Leu
 210 215 220

Asn Asn Leu Ala Val Leu Tyr Gly Lys Arg Gly Lys Tyr Lys Glu Ala
 225 230 235 240

Glu Pro Leu Cys Gln Arg Ala Leu Glu Ile Arg Glu Lys Val Leu Gly
 245 250 255

Thr Asn His Pro Asp Val Ala Lys Gln Leu Asn Asn Leu Ala Leu Leu
 260 265 270

Cys Gln Asn Gln Gly Lys Tyr Glu Ala Val Glu Arg Tyr Tyr Gln Arg
 275 280 285

Ala Leu Ala Ile Tyr Glu Gly Gln Leu Gly Pro Asp Asn Pro Asn Val
 290 295 300

Ala Arg Thr Lys Asn Asn Leu Ala Ser Cys Tyr Leu Lys Gln Gly Lys
 305 310 315 320

Tyr Ala Glu Ala Glu Thr Leu Tyr Lys Glu Ile Leu Thr Arg Ala His
 325 330 335

Val Gln Glu Phe Gly Ser Val Asp Asp Asp His Lys Pro Ile Trp Met
 340 345 350

His Ala Glu Glu Arg Glu Glu Met Ser Lys Ser Arg His His Glu Gly
 355 360 365

Gly Thr Pro Tyr Ala Glu Tyr Gly Ala Trp Val Pro Pro Pro Pro Gln
 370 375 380

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 385 390 395

<210> 92

<211> 785

<212> PRT

<213> Homo sapiens

<400> 92

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 20 25 30

Leu Arg Leu Ser Tyr Arg Asp Leu Leu Ser Ala Asn Arg Ser Ala Ile
 35 40 45

Phe Leu Gly Pro Gln Gly Ser Leu Asn Leu Gln Ala Met Tyr Leu Asp
 50 55 60

Glu Tyr Arg Asp Arg Leu Phe Leu Gly Gly Leu Asp Ala Leu Tyr Ser
 65 70 75 80

Leu Arg Leu Asp Gln Ala Trp Pro Asp Pro Arg Glu Val Leu Trp Pro
 85 90 95

Pro Gln Pro Gly Gln Arg Glu Glu Cys Val Arg Lys Gly Arg Asp Pro
 100 105 110

Leu Thr Glu Cys Ala Asn Phe Val Arg Val Leu Gln Pro His Asn Arg
 115 120 125

Thr His Leu Leu Ala Cys Gly Thr Gly Ala Phe Gln Pro Thr Cys Ala
 130 135 140

Leu Ile Thr Val Gly His Arg Gly Glu His Val Leu His Leu Glu Pro
 145 150 155 160

Gly Ser Val Glu Ser Gly Arg Gly Arg Cys Pro His Glu Pro Ser Arg
 165 170 175

Pro Phe Ala Ser Thr Phe Ile Asp Gly Glu Leu Tyr Thr Gly Leu Thr
 180 185 190

Ala Asp Phe Leu Gly Arg Glu Ala Met Ile Phe Met Ile Phe Arg Ser
 195 200 205

Gly Gly Pro Arg Pro Ala Leu Arg Ser Asp Ser Asp Gln Ser Leu Leu
 210 215 220

His Asp Pro Arg Phe Val Met Ala Ala Arg Ile Pro Glu Asn Ser Asp

225	230	235	240
Gln Asp Asn Asp Lys Val Tyr Phe Phe Phe Ser Glu Thr Val Pro Ser	245	250	255
Pro Asp Gly Gly Ser Asn His Val Thr Val Ser Arg Val Gly Arg Val	260	265	270
Cys Val Asn Asp Ala Gly Gly Gln Arg Val Leu Val Asn Lys Trp Ser	275	280	285
Thr Phe Leu Lys Ala Arg Leu Val Cys Ser Val Pro Gly Pro Gly Gly	290	295	300
Ala Glu Thr His Phe Asp Gln Leu Glu Asp Val Phe Leu Leu Trp Pro	305	310	315
Lys Ala Gly Lys Ser Leu Glu Val Tyr Ala Leu Phe Ser Thr Val Ser	325	330	335
Ala Val Phe Gln Gly Phe Ala Val Cys Val Tyr His Met Ala Asp Ile	340	345	350
Trp Glu Val Phe Asn Gly Pro Phe Ala His Arg Asp Gly Pro Gln His	355	360	365
Gln Trp Gly Pro Tyr Gly Gly Lys Val Pro Phe Pro Arg Pro Gly Val	370	375	380
Cys Pro Ser Lys Met Thr Ala Gln Pro Gly Arg Pro Phe Gly Ser Thr	385	390	395
Lys Asp Tyr Pro Asp Glu Val Leu Gln Phe Ala Arg Ala His Pro Leu	405	410	415
Met Phe Trp Pro Val Arg Pro Arg His Gly Arg Pro Val Leu Val Lys	420	425	430
Thr His Leu Ala Gln Gln Leu His Gln Ile Val Val Asp Arg Val Glu	435	440	445
Ala Glu Asp Gly Thr Tyr Asp Val Ile Phe Leu Gly Thr Asp Ser Gly	450	455	460
Ser Val Leu Lys Val Ile Ala Leu Gln Ala Gly Gly Ser Ala Glu Pro	465	470	475
Glu Glu Val Val Leu Glu Glu Leu Gln Val Phe Lys Val Pro Thr Pro	485	490	495
Ile Thr Glu Met Glu Ile Ser Val Lys Arg Gln Met Leu Tyr Val Gly	500	505	510
Ser Arg Leu Gly Val Ala Gln Leu Arg Leu His Gln Cys Glu Thr Tyr	515	520	525
Gly Thr Ala Cys Ala Glu Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala	530	535	540
Trp Asp Gly Ala Ser Cys Thr His Tyr Arg Pro Ser Leu Gly Lys Arg			

545 550 555 560
 Arg Phe Arg Arg Gln Asp Ile Arg His Gly Asn Pro Ala Leu Gln Cys
 565 570 575
 Leu Gly Gln Ser Gln Glu Glu Glu Ala Val Gly Leu Val Ala Ala Thr
 580 585 590
 Met Val Tyr Gly Thr Glu His Asn Ser Thr Phe Leu Glu Cys Leu Pro
 595 600 605
 Lys Ser Pro Gln Ala Ala Val Arg Trp Leu Leu Gln Arg Pro Gly Asp
 610 615 620
 Glu Gly Pro Asp Gln Val Lys Thr Asp Glu Arg Val Leu His Thr Glu
 625 630 635 640
 Arg Gly Leu Leu Phe Arg Arg Leu Ser Arg Phe Asp Ala Gly Thr Tyr
 645 650 655
 Thr Cys Thr Thr Leu Glu His Gly Phe Ser Gln Thr Val Val Arg Leu
 660 665 670
 Ala Leu Val Val Ile Val Ala Ser Gln Leu Asp Asn Leu Phe Pro Pro
 675 680 685
 Glu Pro Lys Pro Glu Glu Pro Pro Ala Arg Gly Gly Leu Ala Ser Thr
 690 695 700
 Pro Pro Lys Ala Trp Tyr Lys Asp Ile Leu Gln Leu Ile Gly Phe Ala
 705 710 715 720
 Asn Leu Pro Arg Val Asp Glu Tyr Cys Glu Arg Val Trp Cys Arg Gly
 725 730 735
 Thr Thr Glu Cys Ser Gly Cys Phe Arg Ser Arg Ser Arg Gly Lys Gln
 740 745 750
 Ala Arg Gly Lys Ser Trp Ala Gly Leu Glu Leu Gly Lys Lys Met Lys
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 Thr
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<211> 277

<212> PRT

<213> Homo sapiens

<400> 93

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Ile Gln Glu Glu Leu Gln Arg Ser Gly Gly Leu Asp His Leu Val Leu
 35 40 45
 Ser Pro Gly Glu Trp Pro Val Ser Asp Asn Thr Ile Met His Ile Ala
 50 55 60
 Thr Ala Glu Ala Leu Thr Thr Asp Tyr Trp Cys Leu Asp Asp Leu Tyr
 65 70 75 80
 Arg Glu Met Val Arg Cys Tyr Val Glu Ile Val Glu Lys Leu Pro Glu
 85 90 95
 Arg Arg Pro Asp Pro Ala Thr Ile Glu Gly Cys Ala Gln Leu Lys Pro
 100 105 110
 Asn Asn Tyr Leu Leu Ala Trp His Thr Pro Phe Asn Glu Lys Gly Ser
 115 120 125
 Gly Phe Gly Ala Ala Thr Lys Ala Met Cys Ile Gly Leu Arg Tyr Trp
 130 135 140
 Lys Pro Glu Arg Leu Glu Thr Leu Ile Glu Val Ser Val Glu Cys Gly
 145 150 155 160
 Arg Met Thr His Asn His Pro Thr Gly Phe Leu Gly Ser Leu Cys Thr
 165 170 175
 Ala Leu Phe Val Ser Phe Ala Ala Gln Gly Lys Pro Leu Val Gln Trp
 180 185 190
 Gly Arg Asp Met Leu Arg Ala Val Pro Leu Ala Glu Glu Tyr Cys Arg
 195 200 205
 Lys Thr Ile Arg His Thr Ala Glu Tyr Gln Glu His Trp Phe Tyr Leu
 210 215 220
 Lys Leu Asn Gly Asn Phe Ile Trp Arg Arg Gly Lys Ser Val Lys Thr
 225 230 235 240
 Gln Lys Ile Lys Pro Ser Ser Pro Thr Ile Met Met Gln Lys Arg Gly
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<210> 94
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 <213> Homo sapiens

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Val Gln Val Arg Phe Gln Lys Asp Leu Glu Ser Asn Ile Phe Asn Gln
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Leu Ser Ala Cys Met Ser Val Ser Pro Ala Met Thr Thr Arg Arg Lys
 35 40 45

Lys Lys Thr Ser Val Val Lys Arg Lys Pro Lys Arg Met Pro Thr Ser
 50 55 60

Leu Cys Trp Met Arg Leu Cys Leu Cys Thr Asp Gly Thr Val Met Arg
 65 70 75 80

Arg Cys Met Leu Ala Ala Ile Asn Ile Gln Gly Glu Glu Ser Ile Ser
 85 90 95

Ser Ser Leu Thr Thr Pro Thr Leu Cys Gly Gly Gln Asn Gln Ser Thr
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<210> 96
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 <213> Homo sapiens

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Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser Lys Glu Arg Val
 35 40 45

Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala Thr Leu Leu Ile
 50 55 60

Leu Asp Ile Cys Glu Asp Asn Val Pro Asp Pro Lys Asp Val Lys Glu
 65 70 75 80

Arg Phe Ser Gly Ser Leu Val Ala Ala Leu Ser Ala Thr Gly Pro Arg
 85 90 95

Phe Leu Ala Tyr Phe Gly Ser Phe Ala Thr Val Gly Leu Leu Trp Phe
 100 105 110

Ala His His Ser Leu Phe Leu His Val Arg Lys Ala Thr Arg Ala Met
 115 120 125

Gly Leu Leu Asn Thr Leu Ser Leu Ala Phe Val Gly Gly Leu Pro Leu
 130 135 140

Ala Tyr Gln Gln Thr Ser Ala Phe Ala Arg Gln Pro Arg Asp Glu Leu
 145 150 155 160

Glu Arg Val Arg Val Ser Cys Thr Ile Ile Phe Leu Ala Ser Ile Phe
 165 170 175

Gln Leu Ala Thr Trp Thr Thr Ala Leu Leu His Gln Ala Glu Thr Leu
 180 185 190

Gln Pro Ser Val Trp Phe Gly Gly Arg Glu His Val Leu Met Phe Arg
 195 200 205

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 <213> Homo sapiens

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 35 40 45

Gly Ser Ser Cys Gly Leu Pro Ser Thr Val Arg Arg Leu Trp Asp Arg
 50 55 60

Thr Glu Ser Leu Ala Ala Cys Gly Ala Pro Val Pro Ala Ala Ala Pro
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Arg Leu Arg Ser Gly Tyr Pro His Pro Arg His Arg Arg Pro Pro Ala
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Pro Pro Thr Ala Ala His Ala Arg Arg Val His Ala Ala Pro Ala Pro
 100 105 110

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 20 25 30
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 35 40 45
 Ile Leu Arg Leu Pro Arg Pro Ala Ala Cys Met Gly Pro Leu Pro Ser
 50 55 60
 Ser Thr Pro Thr Leu Arg Met Val Pro Cys Ser Ala Leu Val Leu Cys
 65 70 75 80
 Trp Pro Leu Pro Ala Thr Pro Thr Leu Arg His Pro Gly Val Val Gly
 85 90 95
 Pro Asn Trp Leu Ala Pro Pro Ser Ala Ala Leu Cys Arg Pro Asp Ala
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 115 120 125
 Pro Pro Ala Lys
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 <213> Homo sapiens

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 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn
 35 40 45
 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu
 50 55 60
 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser
 65 70 75 80
 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp
 85 90 95
 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp
 100 105 110

Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu
 115 120 125
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln
 130 135 140
 Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val
 145 150 155 160
 Ile Leu Lys Ser Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His
 165 170 175
 Trp Gly Leu Tyr Ile Phe Ser Leu Ala Gln Leu Phe Tyr Thr Thr Val
 180 185 190
 Leu Val Leu Cys Tyr Val Ile Tyr Phe Thr Lys Leu Leu Gly Ser Pro
 195 200 205
 Glu Ser Thr Lys Leu Gln Thr Leu Pro Val Ser Arg Ile Thr Asp Leu
 210 215 220
 Leu Pro Asn Ile Thr Arg Asn Gly Ala Phe Ile Asn Trp Lys Glu Ala
 225 230 235 240
 Lys Leu Thr Trp Ser Phe Phe Lys Gln Ser Phe Leu Lys Gln Ile Leu
 245 250 255
 Thr Glu Gly Glu Arg Tyr Val Met Thr Phe Leu Asn Val Leu Asn Phe
 260 265 270
 Gly Asp Gln Gly Val Tyr Asp Ile Val Asn Asn Leu Gly Ser Leu Val
 275 280 285
 Ala Arg Leu Ile Phe Gln Pro Ile Glu Glu Ser Phe Tyr Ile Phe Phe
 290 295 300
 Ala Lys Val Leu Glu Arg Gly Lys Asp Ala Thr Leu Gln Lys Gln Glu
 305 310 315 320
 Asp Val Ala Val Ala Ala Val Leu Glu Ser Leu Leu Lys Leu Ala
 325 330 335
 Leu Leu Ala Gly Leu Thr Ile Thr Phe Trp Leu Cys Leu Phe Ser Ala
 340 345 350
 Gly Ser Gly Tyr Leu Arg Arg Thr Met Leu Ser Ser Asp Pro Val Phe
 355 360 365
 Leu Cys Cys Glu Gln Ala Gly Gln Pro Asp Trp Ala His Ile Ala Val
 370 375 380
 Gly Ala Phe Cys Leu Gly Ala Thr Leu Gly Thr Ala Phe Leu Thr Glu
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 Thr Lys Leu Ile His Phe Leu Arg Thr Gln Leu Gly Val Pro Arg Arg
 405 410 415
 Thr Asp Lys Met Thr
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<210> 100
<211> 86
<212> PRT
<213> Homo sapiens

<400> 100

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20 25 30
Lys Arg Met Cys Phe Lys Ser Pro Leu Gly Gln Ala Leu Cys Ser Leu
35 40 45
Ala Ser Ser Ser Leu Thr Gln Asp Leu Phe Lys Glu Lys Lys Lys Lys
50 55 60
Thr Trp Ser Leu Lys Pro Arg Ile Asn Ser Ser His Leu Gly Glu Pro
65 70 75 80
Ala Asp Thr Tyr Ser Leu
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<210> 101
<211> 86
<212> PRT
<213> Homo sapiens

<400> 101

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Leu Glu Pro Ser Phe Leu Phe Leu Leu Phe Trp Glu Leu Tyr Cys Val
20 25 30
Cys Cys Gly Met Phe Thr His Thr Ser Cys Cys Leu Gly Phe Leu Gln
35 40 45
Val Val Cys Val Phe Tyr Leu Pro Leu Leu Ala Phe Arg Cys Leu Glu
50 55 60
Ser Met Thr Leu Ala Tyr Ser Ser Val Tyr Ser Arg Arg Pro Cys Leu
65 70 75 80
Phe Leu Ala Phe Ile Lys
85

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/04340

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) :Please See Extra Sheet.

US CL :536/23.1; 435/69.1, 320.1, 252.3, 325; 530/300, 350

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1; 435/69.1, 320.1, 252.3, 325; 530/300, 350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Genbank/EMBL nucleotide and protein sequence databases, STN, MEDLINE, CAS, BIOSIS, EMBASE, SCISEARCH
search terms: bai-3, shiratsuchi, nakamura, tokino

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JP 11-032766 A (OHTSUKA PHARMACEUTICAL CO.) 09 February 1999, see entire document.	1-7
X	Database Genbank Nucleic Acid, NCBI, Accession Number AB005299, SHIRATSUCHI et al. 'Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-specific angiogenesis inhibitor 1 (BAI 1),' Cytogenet. Cell. Genet. 1997, Vol. 79, No. 1-2, pages 103-108.	1-3
--		-----
Y		4-7
X	Database Genbank Protein, NCBI, Accession Number BAA25363, SHIRATSUCHI et al. 'Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-specific angiogenesis inhibitor 1 (BAI 1),' Cytogen. Cell. Genet., 1997, Vol. 79, pages 103-108.	1-3
--		----
Y		4-7

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

A document defining the general state of the art which is not considered to be of particular relevance

E earlier document published on or after the international filing date

L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

&

document member of the same patent family

Date of the actual completion of the international search

04 MAY 2000

Date of mailing of the international search report

24 MAY 2000

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

Peter Brunovskis
PETER BRUNOVSKIS, PH.D.

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/04340

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-8

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/04340

A. CLASSIFICATION OF SUBJECT MATTER: IPC (7):

C12N 1/21, 5/10, 15/12, 15/62, 15/63, 21/00; C07H 21/00; C12P 21/00

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-8, drawn to a polynucleotide, cells containing a polynucleotide, and use of the polynucleotide for producing a protein.

Group II, claims 9-11, drawn to a protein.

Groups III, V, VII, IX, XI, XIII, XV, XVII, XIX, XXI, XXIII, XXV, XXVII, XXIX, XXXI, XXXIII, XXXV, XXXVII, XXXIX, XLI, XLIII, XLV, XLVII, XLVIX, LI, LIII, LV, LVII, LIX, LXI, claims 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, respectively, drawn to polynucleotides.

Groups IV, VI, VIII, X, XII, XIV, XVI, XVIII, XX, XXII, XXIV, XXVI, XXVIII, XXX, XXXII, XXXIV, XXXVI, XXXVIII, XL, XLII, XLIV, XLVI, XLVIII, L, LII, LIV, LVI, LVIII, LX, LXII, claims 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, respectively, drawn to proteins.

The inventions listed as Groups I-LXII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: There is no special technical feature in the first invention of claims 1-8 that is shared by the inventions of Groups II-LXII. Group I does not share any special technical feature with Group II because it does not embrace the same scope of embodiments as the invention of Group II, since most of the embodiments of Group I do not code for proteins; the vast majority of embodiments embracing steps (i)-(k) of claim 1 (and all subsequent even numbered claims beginning with claim 12) either include non-protein encoding polynucleotides with multiple frameshifts or termination codons (steps (j), (k)) or they comprise polynucleotides coding for a protein carrying only a small part of the protein of Group II (step (i)). This same reasoning applies to the other odd numbered Groups (i.e. nucleotides) and each of the even-numbered groups (i.e. proteins) immediately following the previous odd-numbered Group. It is further noted that there is no special technical feature shared by any of the polynucleotides of the odd-numbered Groups, nor is there any special technical feature shared by any of the proteins of the even-numbered Groups. These are independent and distinct inventions.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 1/21, 5/10, 15/12, 15/62, 15/63, C07H 21/00, C12P 21/00		A1	(11) International Publication Number: WO 00/49134
(21) International Application Number: PCT/US00/04340		(43) International Publication Date: 24 August 2000 (24.08.00)	
(22) International Filing Date: 18 February 2000 (18.02.00)			
(30) Priority Data: 60/120,680 19 February 1999 (19.02.99) US 09/298,733 23 April 1999 (23.04.99) US 60/149,639 17 August 1999 (17.08.99) US 60/155,686 23 September 1999 (23.09.99) US 60/157,247 1 October 1999 (01.10.99) US 60/167,823 29 November 1999 (29.11.99) US 60/167,822 29 November 1999 (29.11.99) US Not furnished 15 February 2000 (15.02.00) US		(74) Agent: SPRUNGER, Suzanne, A.; American Home Products Corporation, Patent & Trademark Dept. - 2B, One Campus Drive, Parsippany, NJ 07054 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
(71) Applicant: ALPHAGENE, INC. [US/US]; 260 West Cummings Park, Woburn, MA 01801 (US).		Published <i>With a revised version of the international search report.</i>	
(72) Inventors: VALENZUELA, Dario; 1081 Hill Road, Boxborough, MA 01719-1010 (US). YUAN, Olive; 292 Mystic Street, Arlington, MA 02174 (US). HOFFMAN, Heidi; 90 Houghton Mill Road, Lunenburg, MA 01462 (US). HALL, Jeff; 4 Alderwood Drive, Stratham, NH 03885 (US). RAPIEJKO, Peter; 63 Old Grafton Road, Upton, MA 01568 (US).		(88) Date of publication of the revised version of the international search report: 26 October 2000 (26.10.00)	
(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM			
(57) Abstract			
<p>The present invention provides secreted proteins and polynucleotides encoding them, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.</p>			

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/04340

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 1/21, 5/10, 15/12, 15/62, 15/63; C07H 21/00; C12P 21/00

US CL : 536/23.1; 435/69.1, 320.1, 252.3, 325; 530/300, 350

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1; 435/69.1, 320.1, 252.3, 325; 530/300, 350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Genbank/EMBL nucleotide and protein sequence databases, STN, MEDLINE, CAS, BIOSIS, EMBASE, SCISEARCH
search terms: bai-3, shiratsuchi, nakamura, tokino

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JP 11-032766 A (OHTSUKA PHARMACEUTICAL CO.) 09 February 1999, see entire document.	1-7
X	Database Genbank Nucleic Acid, NCBI, Accession Number AB005299, SHIRATSUCHI et al. 'Cloning and characterization fo	1-3
--	BAI2 and BAI3, novel genes homologous to brain-specific	----
Y	angiogenesis inhibitor 1 (BAI 1),' Cytogenet. Cell. Genet. 1997, Vol. 79, No. 1-2, pages 103-108.	4-7
X	Database Genbank Protein, NCBI, Accession Number BAA25363, SHIRATSUCHI et al. 'Cloning and characterization of BAI2 and	1-3
--	BAI3, novel genes homologous to brain-specific angiogenesis	----
Y	inhibitor 1 (BAI 1),' Cytogen. Cell. Genet., 1997, Vol. 79, pages 103-108.	4-7

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

04 MAY 2000

Date of mailing of the international search report

15 AUG 2000

Name and mailing address of the ISA/US
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Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/04340

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-8

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/04340A. CLASSIFICATION OF SUBJECT MATTER:
IPC (7):

C12N 1/21, 5/10, 15/12, 15/62, 15/63 ; C07H 21/00; C12P 21/00

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-8, drawn to a polynucleotide, cells containing a polynucleotide, and use of the polynucleotide for producing a protein.

Group II, claims 9-11, drawn to a protein.

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Groups IV, VI, VIII, X, XII, XIV, XVI, XVIII, XX, XXII, XXIV, XXVI, XXVIII, XXX, XXXII, XXXIV, XXXVI, XXXVIII, XL, XLII, XLIV, XLVI, XLVIII, L, LII, LIV, LVI, LVIII, LX, LXII, claims 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, respectively, drawn to proteins.

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